

PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 17
ID ABU89831 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 18
ID ABR68080 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 19
ID ADA57044 standard; protein; 266 AA.
DE Human secreted protein #327.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 20
ID ABU60483 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 21
ID ABU96133 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 22
ID ABU92564 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 23
ID ABO08641 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 24
ID ABO02693 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 25
ID ABR74847 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 26
ID ABR94609 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044926-A1.

PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 27
ID ABU13865 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 28
ID ABU85582 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 29
ID ABU98742 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 30
ID ABU97957 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 31
ID ABU91663 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 32
ID ABU89356 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 33
ID ABU86197 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 34
ID ABU67410 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 35
ID ABU80438 standard; protein; 266 AA.
DE Human PRO protein #5.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 36
ID ABU72450 standard; protein; 266 AA.

GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: August 26, 2005, 16:48:35 ; Search time 166 Seconds
(without alignments)
619.749 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWFFQQLSFLPSALVWTS.....YDTAPCPINNERTRLLSRDI 266
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV66636	standard;	protein;	266	AA.	
DE	Membrane-bound	protein	PRO180.			
PN	WO9963088-A2.					
PD	09-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1392;	DB 3;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 4.1e-149;				
RESULT 2						
ID	AAU29028	standard;	protein;	266	AA.	
DE	Human PRO polypeptide	sequence #5.				
PN	WO200168848-A2.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1392;	DB 4;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 4.1e-149;				
RESULT 3						
ID	AAM39568	standard;	protein;	266	AA.	
DE	Human polypeptide	SEQ ID NO 2713.				
PN	WO200153312-A1.					
PD	26-JUL-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1392;	DB 4;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 4.1e-149;				
RESULT 4						
ID	AAB65159	standard;	protein;	266	AA.	
DE	Human PRO180 (UNQ154)	protein sequence	SEQ ID NO:23.			
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1392;	DB 4;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 4.1e-149;				
RESULT 5						
ID	ABB90338	standard;	protein;	266	AA.	
DE	Human polypeptide	SEQ ID NO 2714.				
PN	WO200190304-A2.					
PD	29-NOV-2001.					
PA	(HUNA-) HUMAN GENOME SCI INC.					
Query Match	100.0%;	Score 1392;	DB 5;	Length 266;		
Best Local Similarity	100.0%;	Pred. No. 4.1e-149;				
RESULT 6						
ID	ABG95851	standard;	protein;	266	AA.	

DE Human secreted/transmembrane protein PRO180.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 5; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 7
ID ABUS8404 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 8
ID ABU87952 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 9
ID ABU84267 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 10
ID ABR66141 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 11
ID ABR65531 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 12
ID ABU99471 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 13
ID ABU57974 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 14
ID ABU59052 standard; protein; 266 AA.
DE Novel human secreted or transmembrane protein PRO180.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 15
ID ABU82564 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 16
ID ABU82710 standard; protein; 266 AA.
DE Human PRO polypeptide #5.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 37
ID ABO00106 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 38
ID ABO33935 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 39
ID ABR99356 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 40
ID ABR98746 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 41
ID ABO16269 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 42
ID ABR92169 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 43
ID ABO18810 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 44
ID ABR78231 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 45
ID ABU71952 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 46
ID ABU84967 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 47
ID ABO00106 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 48
ID ABO11438 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 49
ID ABO02083 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 50
ID ADA40898 standard; protein; 266 AA.
DE Human secreted protein.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 51
ID ABU88657 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 52
ID ABU83352 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 53
ID ABO06153 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 54
ID ABR59189 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 55
ID ABO09251 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 56
ID ABO19115 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 57
ID ABO11133 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 58
ID ABR66751 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 59
ID ABO15964 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 60
ID ABO13670 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 61
ID ABU71506 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 62
ID ABU65573 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, SEQ ID 10.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 63
ID ABO07421 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 64
ID ABO03608 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 65
ID ABR67056 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 66
ID ABO13980 standard; protein; 266 AA.
DE Novel human secreted protein #9.

PN US2003038003-A1.
PD 06-FEB-2003.
PA (ROSE/) ROSEN C A.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJJ/) NI J.
PA (WEIY/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAFI/) LAFLEUR D W.
PA (SHIY/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
PA (BIRS/) BIRSE C E.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 67
ID ABO15659 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 68
ID ABU55940 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, PRO180.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 69
ID ABU72287 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 70
ID ABU65268 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 71
ID ABU95213 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 72
ID ABU71116 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 73
ID ABO07726 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 74
ID ABR69967 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 75
ID ABR69300 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 76
ID ABO01441 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 77
ID ABU81243 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 78
ID ABR60040 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 79
ID ABU90960 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 80
ID ABR67775 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 81
ID ABR65163 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 82
ID ABR68385 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 83
ID ABR71797 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 84

ID ABU59199 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 85
ID ABU85277 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 86
ID ABU88967 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 87
ID ABU83047 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 88
ID ABU94903 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 89
ID ABU90451 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 90
ID ABU83962 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 91
ID ABU93613 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 92
ID ABO25896 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 93
ID ABR64858 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 94
ID ABO27281 standard; protein; 266 AA.

DE Human secreted/transmembrane polypeptide PRO180.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 95
ID ABR68690 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 96
ID ABO06506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 97
ID ABR99051 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 98
ID ABU56935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 99
ID ABU85887 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 100
ID ABU82174 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 101
ID ABU87185 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 102
ID ABU83657 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 103
ID ABO08031 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 104
ID ABU92476 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003045684-A1.

PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 105
ID ABU81742 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 106
ID ABU65906 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 107
ID ABU81146 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 108
ID ABR59735 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 109
ID ABU93923 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 110
ID ABU99776 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 111
ID ABR66446 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 112
ID ABR90864 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 113
ID ABO53261 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 114
ID ABU58905 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, #9.

PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 115
ID ABU94291 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 116
ID ABU79173 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 117
ID ABU86502 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 118
ID ABU86807 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 119
ID ABU94596 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 120
ID ABO04523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 121
ID ABR70272 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 122
ID ABU92283 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 123
ID ABU98437 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 124
ID ABR65836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036165-A1.
PD 20-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 125
ID ABR64553 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 126
ID ABU59348 standard; protein; 266 AA.
DE Novel human secreted or transmembrane protein PRO180.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 127
ID ABU79478 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 128
ID ABU92869 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 129
ID ABU95828 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 130
ID ABU91048 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 131
ID ABU90141 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 132
ID ABO09556 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 133
ID ABO10828 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 134
ID ABR70882 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 135
ID ABU98263 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 136
ID ABU87490 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 137
ID ABU91358 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 138
ID ABU89268 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 139
ID ABU84572 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 140
ID ABR69662 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 141
ID ABU80039 standard; protein; 266 AA.
DE Human PRO protein #5.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 142
ID ABU82475 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 143
ID ABU92114 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 144
ID ABU93308 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 145
ID ABO09861 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 146
ID ABO08946 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 147
ID ABU96439 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 148
ID ABU10820 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 149
ID ABU10514 standard; protein; 266 AA.
DE Human secreted/transmembrane protein #5.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 150
ID ABU81572 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 151
ID ABU72109 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 152
ID ABU95523 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 153
ID ABU96732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 154
ID ABR70577 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040076-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 155
ID ABO04928 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 156
ID ABO08336 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 157
ID ABU88511 standard; protein; 266 AA.
DE Human secreted and transmembrane polypeptide PRO180.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 158
ID ABO34025 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 159
ID ABO05543 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 160
ID ABR73932 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 161
ID ABR95524 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 162
ID ABR80821 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 163
ID ABR81126 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 164
ID ABM00822 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 165
ID ABR88424 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 166
ID ABM77245 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 167
ID ABO28729 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 168
ID ABO31474 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 169
ID ABM07891 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 170
ID ABO40371 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 171
ID ABO35796 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 172
ID ABO43935 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 173
ID ADA77762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 174
ID ABM24730 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 175
ID ABO02998 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 176
ID ABR90254 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 177
ID ABM17168 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 178
ID ABR94914 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 179
ID ABR95219 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 180
ID ADB17059 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 181
ID ABO21457 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 182
ID ABR97721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 183
ID ABR87509 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 184
ID ABM77550 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 185
ID ABM27780 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 186
ID ABM06061 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 187
ID ABM03567 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 188
ID ABM35018 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 189
ID ABM26255 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 190
ID ABO48037 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 191
ID ABR92779 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 192
ID ABO24540 standard; protein; 266 AA.

DE Human secreted/transmembrane protein (PRO) #5.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 193
ID ADA37534 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 194
ID ABM11551 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 195
ID ABM02652 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 196
ID ABM15948 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 197
ID ABO27509 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 198
ID ABM29000 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 199
ID ABM06976 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 200
ID ABM21070 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 201
ID ABM09416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 202
ID ABO41286 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 203
ID ABO36101 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 204
ID ABO43630 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 205
ID ABM76330 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 206
ID ABM76026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 207
ID ABM25645 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 208
ID ABM25950 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 209
ID ADA21220 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003054404-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 210
ID ABO03303 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 211

ID ABO02388 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 212
ID ABO44239 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 213
ID ABR90559 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 214
ID ABR73627 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 215
ID ABO16879 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 216
ID ABR94304 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 217
ID ABR75811 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 218
ID ABR71187 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 219
ID ABR93084 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 220
ID ABR93389 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 221
ID ADA10007 standard; protein; 266 AA.
DE Human secreted/transmembrane protein, PRO180.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 222
ID ABR87814 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 223
ID ABO27814 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 224
ID ABO29949 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 225
ID ABO33158 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 226
ID ABM04846 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 227
ID ABM08806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 228
ID ABO36406 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 229
ID ABO35491 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 230
ID ABO39456 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 231
ID ABM10331 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 232
ID ABM11856 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 233
ID ABO52002 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 234
ID ABO52307 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 235
ID ADA19864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 236
ID ABO23625 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 237
ID ADB17247 standard; protein; 266 AA.
DE Human transmembrane PRO polypeptide (SeqID 2).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 238
ID ADA17551 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 239
ID ABR97111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 240
ID ABR86899 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 241
ID ABM10941 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 242
ID ABM28085 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 243
ID ABO32084 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 244
ID ABM15211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 245
ID ABM06366 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 246
ID ABM04177 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 247
ID ABM22290 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 248
ID ABM07586 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068751-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 249
ID ABO40676 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 250
ID ABM35323 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 251
ID ABM33086 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 252
ID ABO52612 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 253
ID ABO50172 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 254
ID ABU99166 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 255
ID ABO04218 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 256
ID ABO05848 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 257
ID ABM18388 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 258

ID ADA27659 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 259
ID ABR97416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 260
ID ABR80516 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 261
ID ABM01127 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 262
ID ABR88729 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 263
ID ABM13381 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 264
ID ABM20765 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 265
ID ABO41896 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 266
ID ABO42506 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 267
ID ABM10026 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003067478-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 268
ID ABO38541 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 269
ID ABM32781 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 270
ID ABM22595 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 271
ID ABM74806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 272
ID ADA79554 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 273
ID ABR96196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 274
ID ABM02347 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 275
ID ABR86289 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 276
ID ABR86594 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 277

ID ABM16558 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 278
ID ABM29610 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 279
ID ABO29034 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 280
ID ABM23815 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 281
ID ABM23205 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 282
ID ABM21985 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 283
ID ABO37626 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 284
ID ABM28390 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 285
ID ABM28695 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 286
ID ABM66339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068737-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 287
ID ABM75721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 288
ID ABM34001 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 289
ID ABM34306 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 290
ID ABO20237 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 291
ID ABO21152 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 292
ID ABO22067 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 293
ID ADA20036 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 294
ID ABO34167 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 295
ID ABR96501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 296
ID ADA94239 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 297
ID ABR85679 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 298
ID ABR99661 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 299
ID ABM00212 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 300
ID ABM00517 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 301
ID ABO29644 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 302
ID ABM23510 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 303
ID ABM29305 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 304
ID ABO38236 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1392; DB 6; Length 266;
RESULT 305
ID ABO45536 standard; protein; 266 AA.
DE Human PRO polypeptide #5.

PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 306
ID ABM20460 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 307
ID ADA81281 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 308
ID ABO16574 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 309
ID ABO18200 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US200304920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 310
ID ABO22627 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 311
ID ABO22932 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 312
ID ABR92474 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 313
ID ABR81431 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 314
ID ABM77855 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 315
ID ABR89644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 316
ID ABM26560 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 317
ID ABM13686 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 318
ID ABO28424 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 319
ID ABO30254 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 320
ID ABM07281 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 321
ID ABM03872 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 322
ID ABO37016 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 323
ID ABO41591 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 324
ID ABO35186 standard; protein; 266 AA.

DE Human PRO polypeptide #5.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 325
ID ABM25035 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 326
ID ABO47427 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 327
ID ABO47732 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 328
ID ABO48342 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 329
ID ABO51392 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 330
ID ABO51697 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 331
ID ABO50477 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 332
ID ABR79601 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 333
ID ABM16863 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040078-A1.
PD 27-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 334
ID ABO17895 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 335
ID ABO20847 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 336
ID ABR96806 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 337
ID ADA38464 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 338
ID ABM12161 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 339
ID ABM16253 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 340
ID ABM24120 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 341
ID ABM14601 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 342
ID ABM04482 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 343
ID ABM06671 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 344
ID ABM09111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 345
ID ABO39151 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 346
ID ABM75416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 347
ID ABM25340 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 348
ID ABM19850 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 349
ID ABO46756 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 350
ID ABO47061 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 351
ID ADA83079 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 352
ID ABR71492 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032133-A1.
PD 13-FEB-2003.

Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 353
ID ABR72102 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 354
ID ABR98441 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 355
ID ABO06811 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 356
ID ABR84764 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 357
ID ABR73322 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 358
ID ABR76416 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 359
ID ABR73017 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 360
ID ABM18083 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 361
ID ABO20542 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 362
ID ABO25285 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 363
ID ABO25590 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 364
ID ABR93999 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 365
ID ADA92585 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003060407-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 366
ID ABR79906 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 367
ID ABM11246 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 368
ID ABO32853 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 369
ID ABO30559 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 370
ID ABO30864 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 371
ID ABM27170 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 372

ID ABM29915 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 373
ID ABM05451 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 374
ID ABM15516 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 375
ID ABM08501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 376
ID ABO42201 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 377
ID ABO37931 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 378
ID ABO45841 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 379
ID ABM66644 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 380
ID ADB20122 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 381
ID ABM19545 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 382
ID ABO49257 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 383
ID ABO49562 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 384
ID ADA78374 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 385
ID ABR88119 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 386
ID ADA00333 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO 180.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 387
ID ABM26865 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 388
ID ABM03262 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 6; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 389
ID ABO39761 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 390
ID ABO49867 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049776-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 391
ID ABO50782 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 392
ID ABO05238 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036126-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 393
ID ABR74542 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 394
ID ABR77021 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 395
ID ABM17778 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 396
ID ABR95829 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 397
ID ABO21762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 398
ID ABO19932 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 399
ID ABO24235 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 400
ID ABR85984 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.

PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 401
ID ABM10636 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 402
ID ABM76635 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 403
ID ABR89339 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 404
ID ABM12466 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 405
ID ABM05756 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 406
ID ABO34881 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 407
ID ABM02957 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 408
ID ABM18935 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 409
ID ABM19240 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104551-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 410
ID ABO46451 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 411
ID ABO48952 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 412
ID ABR68995 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 413
ID ABR89034 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 414
ID ABR72407 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 415
ID ABR74237 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 416
ID ABO18505 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 417
ID ABR80211 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 418
ID ABM01432 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 419
ID ABM02042 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 420
ID ABR87204 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 421
ID ABM12771 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 422
ID ABM30525 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 423
ID ABM24425 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 424
ID ABO29339 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 425
ID ABO31169 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 426
ID ABM14296 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 427
ID ABM09721 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 428
ID ABO38846 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 429
ID ABM34611 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104538-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 430
ID ABO51087 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 431
ID ABO03913 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036158-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 432
ID ABO10383 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003036151-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 433
ID ABO53111 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003044806-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 434
ID ABR77626 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040067-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 435
ID ABR78836 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054456-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 436
ID ABO23930 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 437
ID ABR93694 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 438
ID ABM01737 standard; protein; 266 AA.

DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 439
ID ABM78160 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 440
ID ABR89949 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 441
ID ADA22146 standard; protein; 266 AA.
DE Human secreted/transmembrane polypeptide PRO180.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 442
ID ABM27475 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 443
ID ABM13076 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 444
ID ABO31779 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 445
ID ABM13991 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 446
ID ABM08196 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 447
ID ABO40066 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068681-A1.
PD 10-APR-2003.

Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 448
ID ABM74501 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 449
ID ABM33696 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 450
ID ABM20155 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 451
ID ABO48647 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 452
ID ABO22481 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 453
ID ABR72712 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 454
ID ABO15354 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 455
ID ABR85069 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 456
ID ABO15049 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 457
ID ABO17184 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.

PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 458
ID ABM17473 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 459
ID ADA06312 standard; protein; 266 AA.
DE Human secreted/transmembrane PRO polypeptide #6.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 460
ID ADA39005 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 461
ID ABR85374 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 462
ID ABM76940 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 463
ID ABO28119 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 464
ID ABM22900 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 465
ID ABM30220 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 466
ID ABM21680 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 467
ID ABM21375 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 468
ID ABM14906 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 469
ID ABO40981 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 470
ID ABO36711 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 471
ID ABO37321 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 472
ID ABM75111 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 473
ID ABM33391 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 474
ID ABO46146 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 475
ID ADA82445 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 476
ID ABO37321 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

ID ADB85575 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 477
ID ADB96031 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 478
ID ABM31745 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 479
ID ABM31135 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 480
ID ADB85753 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 481
ID ABM32050 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 482
ID ABM32355 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 483
ID ADB68254 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 484
ID ADB68061 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 485
ID ABM31440 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068761-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 486
ID ABM30830 standard; protein; 266 AA.
DE Human secreted polypeptide PRO180, SEQ ID NO:10.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 487
ID ADB90878 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 488
ID ADC57503 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 489
ID ADC54867 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 490
ID ADC11734 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 491
ID ADC06958 standard; protein; 266 AA.
DE Human PRO180 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 492
ID ADC56156 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 493
ID ADC17137 standard; protein; 266 AA.
DE Mammalian PRO polypeptide (SeqID 2).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 494
ID ADC07211 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 495
ID ADC11201 standard; protein; 266 AA.

DB Human secreted/transmembrane protein PRO180.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 496
ID ADC14835 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 497
ID ADC52330 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 498
ID ADC14323 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 499
ID ADD07855 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 500
ID ADC81680 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 501
ID ADD07322 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 502
ID ADC82213 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 503
ID ADD05483 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 504
ID ADC78249 standard; protein; 266 AA.
DE Human secreted protein SEQ ID NO:56.
PN WO2003072761-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 505
ID ADD08393 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 506
ID ADD06642 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 507
ID ADC82889 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 508
ID ADD54996 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 509
ID ADD36006 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 510
ID ADD55954 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 511
ID ADD54392 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 512
ID ADE26546 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 513
ID ADE26013 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 514
ID ADF66950 standard; protein; 266 AA.
DE Human PRO180 amino acid sequence SEQ ID NO:23.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;

Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 515
ID ADG01007 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 516
ID ADG08560 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 517
ID ADG02478 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 518
ID ADG01185 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 519
ID ADF95360 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 520
ID ADF95181 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 521
ID ADG12175 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 522
ID ADH24034 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 523
ID ADH34060 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 524

ID ADH29893 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 525
ID ADH23864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 526
ID ADH08835 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 527
ID ADG85268 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 528
ID ADH24544 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 529
ID ADH37400 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 530
ID ADH01989 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 531
ID ADH37570 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 532
ID ADG85608 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 533
ID ADH24204 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 534
ID ADH38498 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 535
ID ADG83619 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 536
ID ADH29427 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 537
ID ADH27543 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 538
ID ADH37740 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 539
ID ADH37917 standard; protein; 266 AA.
DE Human secreted and transmembrane protein PRO180.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 540
ID ADH57337 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 541
ID ADH53479 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 542
ID ADH53649 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.

PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 543
ID ADH51985 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 544
ID ADH49840 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 545
ID ADI25350 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 546
ID ADH90143 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 547
ID ADI25520 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 548
ID ADH97694 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 549
ID ADI35204 standard; protein; 266 AA.
DE Human PRO polypeptide #6.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 550
ID ADI03542 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 551
ID ADI11899 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181686-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 552
ID ADH89973 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 553
ID ADH99696 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 554
ID ADH98374 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 555
ID ADI11049 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 556
ID ADI11559 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 557
ID ADH98204 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 558
ID ADH98544 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 559
ID ADH98034 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 560
ID ADI05022 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 561
ID ADI03372 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 562
ID ADI04767 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 563
ID ADH78221 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 564
ID ADI19565 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 565
ID ADH90313 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 566
ID ADI03032 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 567
ID ADH77881 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 568
ID ADH97864 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 569
ID ADI01249 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 570
ID ADI01249 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 570
ID ADI01944 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181652-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 571
ID ADI03202 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 572
ID ADI11389 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 573
ID ADI02291 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 574
ID ADI11729 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 575
ID ADI05366 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 576
ID ADH79438 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 577
ID ADI19395 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 578
ID ADI05196 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 579

ID ADH79608 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 580
ID ADI01434 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 581
ID ADI01604 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 582
ID ADI01774 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 583
ID ADH79778 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 584
ID ADI04596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 585
ID ADI02732 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 586
ID ADH78051 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 587
ID ADI25690 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 588
ID ADI25860 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 589
ID ADK65372 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 590
ID ADH98714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 591
ID ADH79955 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 592
ID ADL32616 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 593
ID ADM30150 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 594
ID ADL93686 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 7; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 595
ID ADC52140 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 596
ID ADE74147 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 597
ID ADE74759 standard; protein; 266 AA.
DE Human secreted/transmembrane protein (PRO) #5.
PN US2003211574-A1.

PD 13-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 598
ID ADF35149 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 599
ID ADG11399 standard; protein; 266 AA.
DE Human PRO180 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 600
ID ADF95972 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 601
ID ADG04243 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 602
ID ADG00403 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 603
ID ADH06572 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 604
ID ADH06402 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 605
ID ADG68823 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 606
ID ADH27713 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;

RESULT 607
ID ADH25054 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 608
ID ADH33686 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 609
ID ADG82659 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 610
ID ADH02329 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 611
ID ADH07936 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 612
ID ADG69333 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 613
ID ADH39154 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 614
ID ADH25940 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 615
ID ADG83894 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 616
ID ADH39324 standard; protein; 266 AA.

ID ADH19269 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 617
ID ADG85438 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 618
ID ADH06232 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 619
ID ADH30063 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 620
ID ADH24374 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 621
ID ADH32909 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 622
ID ADG69503 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 623
ID ADH07766 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 624
ID ADG85778 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 625
ID ADH39324 standard; protein; 266 AA.

DE Novel human secreted and transmembrane protein PRO180.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 626
ID ADH33516 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 627
ID ADH33856 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 628
ID ADH01066 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 629
ID ADG69673 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 630
ID ADH20762 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003224358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 631
ID ADH02159 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 632
ID ADG69163 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 633
ID ADG85948 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 634
ID ADH24884 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180909-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 635
ID ADH39501 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 636
ID ADH19802 standard; protein; 266 AA.
DE Human secreted/transmembrane protein PRO180.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 637
ID ADH02499 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 638
ID ADG68993 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 639
ID ADH07596 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 640
ID ADG86118 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 641
ID ADH24714 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 642
ID ADH25762 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 643
ID ADH38328 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2003180922-A1.
PD 25-SEP-2003.

Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 662
ID ADJ64419 standard; protein; 266 AA.
DE Human PRO polypeptide #5.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 663
ID ADM31315 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 664
ID ADM36362 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 665
ID ADM40167 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 666
ID ADM80857 standard; protein; 266 AA.
DE Human PRO polypeptide #1.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 667
ID ADN60677 standard; protein; 266 AA.
DE Human secreted polypeptide #9.
PN US2004038277-A1.
PD 26-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 668
ID ADN37775 standard; protein; 266 AA.
DE Novel human secreted and transmembrane protein PRO180.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1392; DB 8; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 669
ID AAY27575 standard; protein; 267 AA.
DE Human secreted protein encoded by gene No. 9.
PN WO9924836-A1.
PD 20-MAY-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1392; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 670
ID ADG78386 standard; protein; 267 AA.
DE Human secreted protein #9.
PN US2003211472-A1.
PD 13-NOV-2003.
PA (FENG/) FENG P.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.

PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (NIJJ/) NI J.
PA (WEIY/) WEI Y.
PA (SOPP/) SOPPET D R.
PA (MOOR/) MOORE P A.
PA (KYAW/) KYAW H.
PA (LAFL/) LAFLEUR D W.
PA (SHIY/) SHI Y.
PA (JANA/) JANAT F.
PA (ENDR/) ENDRESS G A.
PA (CART/) CARTER K C.
Query Match 100.0%; Score 1392; DB 8; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.1e-149;
RESULT 671
ID ABB12041 standard; peptide; 275 AA.
DE Human secreted protein homologue, SEQ ID NO:2411.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1392; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
RESULT 672
ID AAM41354 standard; protein; 275 AA.
DE Human polypeptide SEQ ID NO 6285.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1392; DB 4; Length 275;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
RESULT 673
ID AAB87526 standard; protein; 266 AA.
DE Human PRO180.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 99.9%; Score 1390; DB 4; Length 266;
Best Local Similarity 99.6%; Pred. No. 6.9e-149;
RESULT 674
ID AAY36185 standard; protein; 267 AA.
DE Human secreted protein #57.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 99.7%; Score 1388; DB 2; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.2e-148;
RESULT 675
ID ADJ46037 standard; protein; 267 AA.
DE Novel human secreted protein-related protein sequence SeqID190.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 99.7%; Score 1388; DB 7; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.2e-148;
RESULT 676
ID ADP19446 standard; protein; 267 AA.
DE Human secreted polypeptide #297.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 99.7%; Score 1388; DB 8; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.2e-148;
RESULT 677
ID AAY29866 standard; protein; 208 AA.
DE Human secreted protein clone pe318_4.
PN WO9946287-A1.
PD 16-SEP-1999.
PA (GEMY) GENETICS INST INC.
Query Match 77.4%; Score 1078; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 1.3e-113;
RESULT 678

ID ABP75476 standard; protein; 166 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 660.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 58.6%; Score 816; DB 6; Length 166;
Best Local Similarity 93.4%; Pred. No. 5.7e-84;
RESULT 679
ID AAB88330 standard; protein; 136 AA.
DE Human membrane or secretory protein clone PSEC0031.
PN EPI067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 52.1%; Score 725; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 9.3e-74;
RESULT 680
ID AAY36138 standard; protein; 172 AA.
DE Human secreted protein #10.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 42.8%; Score 595.5; DB 2; Length 172;
Best Local Similarity 79.4%; Pred. No. 6.6e-59;
RESULT 681
ID ADJ45943 standard; protein; 172 AA.
DE Novel human secreted protein-related protein sequence SeqID96.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLEERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 42.8%; Score 595.5; DB 7; Length 172;
Best Local Similarity 79.4%; Pred. No. 6.6e-59;
RESULT 682
ID ADM04182 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:2867.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 34.9%; Score 486.5; DB 7; Length 238;
Best Local Similarity 38.6%; Pred. No. 2.5e-46;
RESULT 683
ID AAE26425 standard; protein; 231 AA.
DE Human transmembrane protein (TMP)-11 protein.
PN WO200234783-A2.
PD 02-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 34.5%; Score 480.5; DB 5; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.1e-45;
RESULT 684
ID ADK70499 standard; protein; 231 AA.
DE Respiratory disease differentially expressed protein #65.
PN WO2003101283-A2.
PD 11-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match 34.5%; Score 480.5; DB 8; Length 231;
Best Local Similarity 38.7%; Pred. No. 1.1e-45;
RESULT 685
ID AAE05342 standard; protein; 238 AA.
DE Mouse secreted protein #1.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 34.4%; Score 479.5; DB 4; Length 238;
Best Local Similarity 37.3%; Pred. No. 1.5e-45;
RESULT 686
ID ABO00865 standard; protein; 246 AA.
DE Polypeptide encoded by novel human contig #116.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 33.2%; Score 461.5; DB 6; Length 246;
Best Local Similarity 39.3%; Pred. No. 1.8e-43;

RESULT 687
ID ABB60356 standard; protein; 246 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7860.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 26.0%; Score 361.5; DB 4; Length 246;
Best Local Similarity 33.6%; Pred. No. 4.1e-32;
RESULT 688
ID AAY36219 standard; protein; 69 AA.
DE Human secreted protein #91.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 689
ID AAY36172 standard; protein; 69 AA.
DE Human secreted protein #44.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.7%; Score 358; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 690
ID ADJ46071 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID224.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLEERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 691
ID ADJ45977 standard; protein; 69 AA.
DE Novel human secreted protein-related protein sequence SeqID130.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLEERT A.
PA (BOUG/) BOUGUELERET L.
Query Match 25.7%; Score 358; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 692
ID ADP19480 standard; protein; 69 AA.
DE Human secreted polypeptide #331.
PN US2004110939-A1.
PD 10-JUN-2004.
PA (GEST) GENSET SA.
Query Match 25.7%; Score 358; DB 8; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.8e-32;
RESULT 693
ID ABG28122 standard; protein; 200 AA.
DE Novel human diagnostic protein #28113.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 25.6%; Score 356.5; DB 4; Length 200;
Best Local Similarity 74.0%; Pred. No. 1.1e-31;
RESULT 694
ID ABB97776 standard; protein; 85 AA.
DE Human secretory polypeptide (SPTM) 28.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 25.6%; Score 356; DB 5; Length 85;
Best Local Similarity 86.1%; Pred. No. 4e-32;
RESULT 695
ID AAY04148 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO:19.
PN WO9906439-A2.
PD 11-FEB-1999.

PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 696
ID AAW93616 standard; protein; 69 AA.
DE Human 5' EST secreted protein clone 58-34-2-E7-FL2.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 697
ID AAY04166 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO:19.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 698
ID AAY35882 standard; protein; 69 AA.
DE Extended human secreted protein sequence, SEQ ID NO. 19.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 699
ID AAY59645 standard; protein; 69 AA.
DE Secreted protein extended EST protein sequence #2.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 700
ID AAY01590 standard; protein; 69 AA.
DE Secreted protein encoded by an extended 5' EST cDNA sequence.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 701
ID AAY12982 standard; protein; 69 AA.
DE Human secreted protein encoded by 5' EST clone 58-34-2-E7-FL2.
PN WO9906552-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 702
ID AAY25451 standard; protein; 69 AA.
DE Human secreted protein 2 derived from extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 703
ID AAY12672 standard; peptide; 69 AA.
DE Human 5' EST secreted protein.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 25.3%; Score 352; DB 2; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 704
ID AAG00010 standard; protein; 69 AA.
DE Human secreted protein #1.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.

Query Match 25.3%; Score 352; DB 3; Length 69;
Best Local Similarity 98.5%; Pred. No. 8.5e-32;
RESULT 705
ID ABB89768 standard; protein; 180 AA.
DE Human polypeptide SEQ ID NO 2144.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.8%; Score 317.5; DB 5; Length 180;
Best Local Similarity 33.3%; Pred. No. 2.6e-27;
RESULT 706
ID AAG81279 standard; protein; 114 AA.
DE Human AFP protein sequence SEQ ID NO:76.
PN WO200129221-A2.
PD 26-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 19.6%; Score 272.5; DB 4; Length 114;
Best Local Similarity 47.5%; Pred. No. 1.8e-22;
RESULT 707
ID AAB93632 standard; protein; 132 AA.
DE Human protein sequence SEQ ID NO:13115.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 18.0%; Score 251; DB 4; Length 132;
Best Local Similarity 33.3%; Pred. No. 6.1e-20;
RESULT 708
ID ADL06520 standard; protein; 132 AA.
DE Human tumour-associated antigenic target (TAT) polypeptide #19.
PN WO2004016225-A2.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 6.1e-20;
RESULT 709
ID ADJ75472 standard; protein; 132 AA.
DE Marker gene related amino acid sequence SEQ ID NO:724.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 6.1e-20;
RESULT 710
ID ADR14452 standard; protein; 132 AA.
DE Human NF-kappaB pathway-associated protein SeqID453.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 6.1e-20;
RESULT 711
ID ADP24981 standard; protein; 132 AA.
DE PRO polypeptide SEQ ID NO:2159.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 18.0%; Score 251; DB 8; Length 132;
Best Local Similarity 33.3%; Pred. No. 6.1e-20;
RESULT 712
ID ADS11008 standard; protein; 233 AA.
DE Human therapeutic protein - SEQ ID 1245.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 15.8%; Score 220.5; DB 8; Length 233;
Best Local Similarity 27.2%; Pred. No. 3.9e-16;
RESULT 713
ID ABO00507 standard; protein; 283 AA.
DE Novel human polypeptide #94.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 15.4%; Score 214.5; DB 6; Length 283;

Best Local Similarity 26.2%; Pred. No. 2.5e-15;
RESULT 714
ID AAB08866 standard; protein; 249 AA.
DE Amino acid sequence of a human secretory protein.
PN WO200052151-A2.
PD 08-SEP-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 15.2%; Score 212; DB 3; Length 249;
Best Local Similarity 26.5%; Pred. No. 4e-15;
RESULT 715
ID AAM38964 standard; protein; 249 AA.
DE Human polypeptide SEQ ID NO 2109.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.2%; Score 212; DB 4; Length 249;
Best Local Similarity 26.5%; Pred. No. 4e-15;
RESULT 716
ID AAM51628 standard; protein; 249 AA.
DE Human plasminogen activator inhibitor 2-27 polypeptide.
PN CNI313331-A.
PD 19-SEP-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 15.2%; Score 212; DB 5; Length 249;
Best Local Similarity 26.5%; Pred. No. 4e-15;
RESULT 717
ID ADP18677 standard; protein; 249 AA.
DE Human protein encoded by TAT414 cDNA used to treat cancer SeqID 37.
PN WO2004045516-A2.
PD 03-JUN-2004.
PA (GETH) GENENTECH INC.
Query Match 15.2%; Score 212; DB 8; Length 249;
Best Local Similarity 26.5%; Pred. No. 4e-15;
RESULT 718
ID AAY12179 standard; protein; 36 AA.
DE Human 5' EST secreted protein SEQ ID NO: 492.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 14.0%; Score 195; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e-14;
RESULT 719
ID AAM40750 standard; protein; 274 AA.
DE Human polypeptide SEQ ID NO 5681.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.8%; Score 192.5; DB 4; Length 274;
Best Local Similarity 31.4%; Pred. No. 7.4e-13;
RESULT 720
ID ABG17213 standard; protein; 308 AA.
DE Novel human diagnostic protein #17204.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.9%; Score 180; DB 4; Length 308;
Best Local Similarity 100.0%; Pred. No. 2.3e-11;
RESULT 721
ID ABG16460 standard; protein; 466 AA.
DE Novel human diagnostic protein #16451.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 12.7%; Score 176.5; DB 4; Length 466;
Best Local Similarity 60.0%; Pred. No. 1e-10;
RESULT 722
ID AAE00332 standard; protein; 253 AA.
DE Human membrane-bound protein-60 alternative mature protein sequence.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 253;
Best Local Similarity 24.5%; Pred. No. 2.9e-09;

RESULT 723
ID AAE00331 standard; protein; 256 AA.
DE Human membrane-bound protein-60 (Zsig60) mature protein sequence.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 256;
Best Local Similarity 24.5%; Pred. No. 2.9e-09;
RESULT 724
ID AAB18985 standard; protein; 271 AA.
DE Amino acid sequence of a human transmembrane protein.
PN WO200056891-A2.
PD 28-SEP-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 11.5%; Score 160.5; DB 3; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.1e-09;
RESULT 725
ID AAE00330 standard; protein; 271 AA.
DE Human membrane-bound protein-60 (Zsig60).
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 11.5%; Score 160.5; DB 4; Length 271;
Best Local Similarity 24.5%; Pred. No. 3.1e-09;
RESULT 726
ID AAY48244 standard; protein; 304 AA.
DE Human prostate cancer-associated protein 30.
PN DE19811193-A1.
PD 16-SEP-1999.
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.
Query Match 10.9%; Score 152; DB 2; Length 304;
Best Local Similarity 24.0%; Pred. No. 3.4e-08;
RESULT 727
ID AAE00334 standard; protein; 160 AA.
DE Human membrane-bound protein-60 alternative mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.9%; Score 151.5; DB 4; Length 160;
Best Local Similarity 29.5%; Pred. No. 1.6e-08;
RESULT 728
ID AAE00333 standard; protein; 163 AA.
DE Human membrane-bound protein-60 (Zsig60) mature extracellular portion.
PN WO200123567-A1.
PD 05-APR-2001.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 10.9%; Score 151.5; DB 4; Length 163;
Best Local Similarity 29.5%; Pred. No. 1.6e-08;
RESULT 729
ID AAY94930 standard; protein; 437 AA.
DE Human secreted protein clone qal36_1 protein sequence SEQ ID NO:66.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 10.9%; Score 151.5; DB 3; Length 437;
Best Local Similarity 26.8%; Pred. No. 6.4e-08;
RESULT 730
ID AAY95013 standard; protein; 178 AA.
DE Human secreted protein vc48_1, SEQ ID NO:66.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 10.6%; Score 147.5; DB 3; Length 178;
Best Local Similarity 24.9%; Pred. No. 5.3e-08;
RESULT 731
ID ADN02727 standard; protein; 255 AA.
DE Human receptor and membrane -associated protein #30.
PN WO2004029218-A2.
PD 08-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.5%; Score 146.5; DB 8; Length 255;
Best Local Similarity 24.6%; Pred. No. 1.1e-07;
RESULT 732

ID ABO00615 standard; protein; 63 AA.
DE Novel human polypeptide #202.
PN WO2003023013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC. 9.1%; Score 126; DB 6; Length 63;
Query Match Best Local Similarity 47.2%; Pred. No. 3.5e-06;
RESULT 733
ID ADS11007 standard; protein; 127 AA.
DE Human therapeutic protein - SEQ ID 1244.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC. 8.8%; Score 122.5; DB 8; Length 127;
Query Match Best Local Similarity 32.1%; Pred. No. 2.3e-05;
RESULT 734
ID AAY04149 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PN WO9906439-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 735
ID AAY11369 standard; protein; 21 AA.
DE Human 5' EST secreted protein SEQ ID NO:20.
PN WO9906551-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 736
ID AAY12516 standard; peptide; 21 AA.
DE Human 5' EST signal peptide SEQ ID NO: 20 from WO 9906553.
PN WO9906553-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 737
ID AAY35883 standard; peptide; 21 AA.
DE Signal peptide of extended secreted protein, SEQ ID NO. 20.
PN WO9931236-A2.
PD 24-JUN-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 738
ID AAY59644 standard; peptide; 21 AA.
DE Secreted protein extended EST signal peptide #2.
PN WO9940189-A2.
PD 12-AUG-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 739
ID AAY25452 standard; peptide; 21 AA.
DE Human secreted protein 2 signal peptide derived from extended cDNA.
PN WO9925825-A2.
PD 27-MAY-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 740
ID AAY12671 standard; peptide; 21 AA.
DE Human 5' EST secreted protein signal peptide.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 741
ID AAY11711 standard; protein; 21 AA.

DE Peptide encoded by extended cDNA derived from 5' EST.
PN WO9906550-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 742
ID AAY64644 standard; peptide; 21 AA.
DE Human 58-34-2-E7-FL2 signal peptide.
PN WO9953051-A2.
PD 21-OCT-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 743
ID AAG00011 standard; peptide; 21 AA.
DE Human secreted protein #1 signal peptide.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 744
ID AAO20328 standard; peptide; 21 AA.
DE Signal peptide encoded by the cDNA 58-34-2-E7-FL2.
PN CA2343602-A1.
PD 18-OCT-2001.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 745
ID ADJ45867 standard; peptide; 21 AA.
DE Novel human secreted protein-related peptide sequence SeqID20.
PN US2003144490-A1.
PD 31-JUL-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLETT A.
PA (BOUG/) BOUGUELERET L.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 746
ID ADM77739 standard; peptide; 21 AA.
DE Signal sequence #2.
PN US2003162176-A1.
PD 28-AUG-2003.
PA (EDWA/) EDWARDS J D M.
PA (DUCL/) DUCLETT A.
PA (BOUG/) BOUGUELERET L.
Query Match Best Local Similarity 100.0%; Pred. No. 6.3e-06;
RESULT 747
ID AAY04167 standard; peptide; 21 AA.
DE Human secreted protein 5' EST signal peptide SEQ ID NO:20.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match Best Local Similarity 95.2%; Pred. No. 2.3e-05;
RESULT 748
ID AAU04087 standard; peptide; 21 AA.
DE Signal peptide encoded by Human cDNA 58-34-2-E7-FL2.
PN EP1104808-A1.
PD 06-JUN-2001.
PA (GEST) GENSET.
Query Match Best Local Similarity 100.0%; Pred. No. 2.3e-05;
RESULT 749
ID ABB60233 standard; protein; 275 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7491.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 7.7%; Score 106.5; DB 4; Length 275;
Query Match

Best Local Similarity 21.3%; Pred. No. 0.0044;
RESULT 750
ID AAB38499 standard; peptide; 220 AA.
DE Fragment of human secreted protein encoded by gene 53 clone HPABG18.
PN WO200061623-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.5%; Score 105; DB 3; Length 220;
Best Local Similarity 22.8%; Pred. No. 0.0048;
RESULT 751
ID AAM93195 standard; protein; 218 AA.
DE Human polypeptide, SEQ ID NO: 2575.
PN EPI130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 7.3%; Score 101; DB 4; Length 218;
Best Local Similarity 22.8%; Pred. No. 0.013;
RESULT 752
ID ADL30542 standard; protein; 218 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2575.
PN EPI396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 101; DB 8; Length 218;
Best Local Similarity 22.8%; Pred. No. 0.013;
RESULT 753
ID ADM06102 standard; protein; 187 AA.
DE Human protein of the invention SEQ ID NO:4787.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 99; DB 7; Length 187;
Best Local Similarity 23.4%; Pred. No. 0.018;
RESULT 754
ID ABU45347 standard; protein; 1066 AA.
DE Protein encoded by Prokaryotic essential gene #30874.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1066;
Best Local Similarity 19.5%; Pred. No. 0.23;
RESULT 755
ID ABU47563 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #33090.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.24;
RESULT 756
ID ABU46980 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #32507.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 98.5; DB 6; Length 1120;
Best Local Similarity 19.5%; Pred. No. 0.24;
RESULT 757
ID ABU34113 standard; protein; 548 AA.
DE Protein encoded by Prokaryotic essential gene #19640.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 94.5; DB 6; Length 548;
Best Local Similarity 18.2%; Pred. No. 0.26;
RESULT 758
ID ABU39811 standard; protein; 269 AA.
DE Protein encoded by Prokaryotic essential gene #25338.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.8%; Score 94; DB 6; Length 269;
Best Local Similarity 21.7%; Pred. No. 0.11;

RESULT 759
ID AAG44537 standard; protein; 303 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55801.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 93.5; DB 3; Length 303;
Best Local Similarity 21.8%; Pred. No. 0.15;
RESULT 760
ID AAG44536 standard; protein; 367 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55800.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 93.5; DB 3; Length 367;
Best Local Similarity 21.8%; Pred. No. 0.19;
RESULT 761
ID ABU15091 standard; protein; 1120 AA.
DE Protein encoded by Prokaryotic essential gene #618.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 93; DB 6; Length 1120;
Best Local Similarity 19.6%; Pred. No. 1;
RESULT 762
ID ABU47616 standard; protein; 473 AA.
DE Protein encoded by Prokaryotic essential gene #33143.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.6%; Score 92.5; DB 6; Length 473;
Best Local Similarity 22.8%; Pred. No. 0.36;
RESULT 763
ID ABB89477 standard; protein; 118 AA.
DE Human polypeptide SEQ ID NO 1853.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.6%; Score 91.5; DB 5; Length 118;
Best Local Similarity 28.0%; Pred. No. 0.069;
RESULT 764
ID ADC94520 standard; protein; 291 AA.
DE E. faecium protein sequence SEQ ID 4147.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.6%; Score 91.5; DB 7; Length 291;
Best Local Similarity 22.9%; Pred. No. 0.24;
RESULT 765
ID ADN23444 standard; protein; 373 AA.
DE Bacterial polypeptide #6097.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.6%; Score 91.5; DB 8; Length 373;
Best Local Similarity 23.0%; Pred. No. 0.34;
RESULT 766
ID AAU03808 standard; protein; 387 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #7.
PN WO200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.6%; Score 91.5; DB 4; Length 387;
Best Local Similarity 23.0%; Pred. No. 0.35;
RESULT 767
ID ABB91939 standard; protein; 712 AA.
DE Herbicidially active polypeptide SEQ ID NO 1150.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.6%; Score 91.5; DB 5; Length 712;

Best Local Similarity 22.2%; Pred. No. 0.82;
RESULT 768
ID ADN46339 standard; protein; 451 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID217.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.5%; Score 90.5; DB 8; Length 451;
Best Local Similarity 21.2%; Pred. No. 0.57;
RESULT 769
ID AAB76803 standard; protein; 283 AA.
DE Corynebacterium glutamicum MCT protein SEQ ID NO:588.
PN WO200100805-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.34;
RESULT 770
ID AAG89779 standard; protein; 283 AA.
DE C glutamicum protein fragment SEQ ID NO: 3533.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.5%; Score 90; DB 4; Length 283;
Best Local Similarity 23.8%; Pred. No. 0.34;
RESULT 771
ID ADP98865 standard; protein; 505 AA.
DE C. albicans specific gene, orf6.4442, protein sequence.
PN WO2004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.5%; Score 90; DB 8; Length 505;
Best Local Similarity 20.5%; Pred. No. 0.75;
RESULT 772
ID ABU45537 standard; protein; 458 AA.
DE Protein encoded by Prokaryotic essential gene #31064.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89.5; DB 6; Length 458;
Best Local Similarity 22.8%; Pred. No. 0.75;
RESULT 773
ID ABP26393 standard; protein; 579 AA.
DE Streptococcus polypeptide SEQ ID NO 1962.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.4%; Score 89.5; DB 5; Length 579;
Best Local Similarity 24.8%; Pred. No. 1;
RESULT 774
ID ABU50406 standard; protein; 428 AA.
DE Protein encoded by Prokaryotic essential gene #35933.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 89; DB 6; Length 428;
Best Local Similarity 21.6%; Pred. No. 0.78;
RESULT 775
ID AAB94689 standard; protein; 637 AA.
DE Human protein sequence SEQ ID NO:15654.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.4%; Score 89; DB 4; Length 637;
Best Local Similarity 21.5%; Pred. No. 1.3;
RESULT 776
ID ABU23408 standard; protein; 642 AA.
DE Protein encoded by Prokaryotic essential gene #8935.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.

Query Match 6.4%; Score 89; DB 6; Length 642;
Best Local Similarity 20.8%; Pred. No. 1.4;
RESULT 777
ID AAU03497 standard; protein; 757 AA.
DE Human sterol sensing domain protein.
PN WO200146227-A2.
PD 28-JUN-2001.
PA (UYZU-) UNIV ZURICH.
Query Match 6.4%; Score 89; DB 4; Length 757;
Best Local Similarity 21.5%; Pred. No. 1.7;
RESULT 778
ID AAB41293 standard; protein; 758 AA.
DE Human ORFX ORF1057 polypeptide sequence SEQ ID NO:2114.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 89; DB 3; Length 758;
Best Local Similarity 21.5%; Pred. No. 1.7;
RESULT 779
ID AAU74820 standard; protein; 1124 AA.
DE Human REPTR 3 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.4%; Score 89; DB 5; Length 1124;
Best Local Similarity 21.5%; Pred. No. 2.9;
RESULT 780
ID ADA55083 standard; protein; 1203 AA.
DE Human protein, SEQ ID 2651.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.4%; Score 89; DB 6; Length 1203;
Best Local Similarity 21.5%; Pred. No. 3.2;
RESULT 781
ID ABG31547 standard; protein; 1330 AA.
DE Human patched-like protein.
PN WO200246402-A2.
PD 13-JUN-2002.
PA (FARB) BAYER AG.
Query Match 6.4%; Score 89; DB 5; Length 1330;
Best Local Similarity 21.5%; Pred. No. 3.7;
RESULT 782
ID AAB96747 standard; protein; 430 AA.
DE Putative P. abyssi permease #26.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 6.4%; Score 88.5; DB 4; Length 430;
Best Local Similarity 23.8%; Pred. No. 0.89;
RESULT 783
ID AAR37309 standard; protein; 1165 AA.
DE Cardiac adenyllyl cyclase.
PN EP543137-A1.
PD 26-MAY-1993.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 6.3%; Score 88; DB 2; Length 1165;
Best Local Similarity 20.5%; Pred. No. 4;
RESULT 784
ID ABU19097 standard; protein; 233 AA.
DE Protein encoded by Prokaryotic essential gene #4624.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 87.5; DB 6; Length 233;
Best Local Similarity 22.8%; Pred. No. 0.5;
RESULT 785
ID ADD67113 standard; protein; 322 AA.
DE Homogentisate prenyl transferase.
PN WO2003080647-A2.
PD 02-OCT-2003.

PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 6.3%; Score 87.5; DB 7; Length 322;
Best Local Similarity 22.6%; Pred. No. 0.78;
RESULT 786
ID ADC77581 standard; protein; 453 AA.
DE Mouse TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.3%; Score 87.5; DB 7; Length 453;
Best Local Similarity 19.9%; Pred. No. 1.2;
RESULT 787
ID ADS28619 standard; protein; 482 AA.
DE Bacterial polypeptide #17652.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.3%; Score 87.5; DB 8; Length 482;
Best Local Similarity 21.2%; Pred. No. 1.4;
RESULT 788
ID ABU33543 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #19070.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86.5; DB 6; Length 239;
Best Local Similarity 20.4%; Pred. No. 0.67;
RESULT 789
ID ADT05661 standard; protein; 261 AA.
DE Haemophilus influenzae (NTHi) protein - SEQ ID 697.
PN WO2004078949-A2.
PD 16-SEP-2004.
PA (CHIL-) CHILDRENS HOSPITAL INC.
Query Match 6.2%; Score 86.5; DB 8; Length 261;
Best Local Similarity 24.2%; Pred. No. 0.76;
RESULT 790
ID ADH87029 standard; protein; 356 AA.
DE Enterococcus faecalis polypeptide #1509.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.2%; Score 86.5; DB 7; Length 356;
Best Local Similarity 19.2%; Pred. No. 1.2;
RESULT 791
ID ADS44642 standard; protein; 400 AA.
DE Bacterial polypeptide #23072.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 86.5; DB 8; Length 400;
Best Local Similarity 21.9%; Pred. No. 1.4;
RESULT 792
ID ABB47717 standard; protein; 583 AA.
DE Listeria monocytogenes protein #421.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.2%; Score 86.5; DB 5; Length 583;
Best Local Similarity 19.4%; Pred. No. 2.3;
RESULT 793
ID AAG39112 standard; protein; 1346 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48347.
PN EP1033405-A2.
PD 06-SEP-2000.

Query Match 6.2%; Score 86.5; DB 3; Length 1346;
Best Local Similarity 18.2%; Pred. No. 7.3;
RESULT 794
ID AAG39111 standard; protein; 1390 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48346.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1390;
Best Local Similarity 18.2%; Pred. No. 7.6;
RESULT 795
ID AAG39110 standard; protein; 1403 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48345.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 86.5; DB 3; Length 1403;
Best Local Similarity 18.2%; Pred. No. 7.7;
RESULT 796
ID ABM73219 standard; protein; 372 AA.
DE Staphylococcus aureus protein #2459.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%; Score 86; DB 6; Length 372;
Best Local Similarity 18.1%; Pred. No. 1.4;
RESULT 797
ID AAG98347 standard; protein; 396 AA.
DE Escherichia coli protein sequence SEQ ID NO:395.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 4; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.5;
RESULT 798
ID ABU14798 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #325.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 86; DB 6; Length 396;
Best Local Similarity 21.9%; Pred. No. 1.5;
RESULT 799
ID ABB90798 standard; protein; 725 AA.
DE Herbicidally active polypeptide SEQ ID NO 9.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.2%; Score 86; DB 5; Length 725;
Best Local Similarity 18.9%; Pred. No. 3.5;
RESULT 800
ID AAB11039 standard; protein; 841 AA.
DE S. xylosoe mprF protein.
PN DE19914817-A1.
PD 05-OCT-2000.
PA (PETR-) PETRY GENMEDICS GMBH.
Query Match 6.2%; Score 86; DB 3; Length 841;
Best Local Similarity 18.3%; Pred. No. 4.3;
RESULT 801
ID ABP77912 standard; protein; 295 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 2354.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.2;
RESULT 802
ID ABU37235 standard; protein; 295 AA.
DE Protein encoded by Prokaryotic essential gene #22762.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 1.2;
RESULT 803

ID ABJ39122 standard; protein; 311 AA.
DE Molecule for disease detection and treatment (MDDT)-32 protein sequence.
PN WO2003052049-A2.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.1%; Score 85.5; DB 6; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.3;
RESULT 804
ID ADC37363 standard; protein; 311 AA.
DE Nuclear factor kappa B (NF-kappaB) activating protein, SEQ ID 196.
PN WO2003048202-A2.
PD 12-JUN-2003.
PA (ASAH) ASahi KASEI KK.
Query Match 6.1%; Score 85.5; DB 7; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.3;
RESULT 805
ID ADR58959 standard; protein; 311 AA.
DE Human Elk1 phosphorylation/Elk1 kinase activation protein - SEQ ID 62.
PN WO2004072277-A2.
PD 26-AUG-2004.
PA (ASAH-) ASahi KASEI PHARMA CORP.
Query Match 6.1%; Score 85.5; DB 8; Length 311;
Best Local Similarity 21.7%; Pred. No. 1.3;
RESULT 806
ID AAM93524 standard; protein; 329 AA.
DE Human polypeptide, SEQ ID NO: 3257.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.4;
RESULT 807
ID AAB92687 standard; protein; 329 AA.
DE Human protein sequence SEQ ID NO:11071.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.4;
RESULT 808
ID ADL31224 standard; protein; 329 AA.
DE Human protein encoded by a full length cDNA clone seqID 3257.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 85.5; DB 8; Length 329;
Best Local Similarity 23.0%; Pred. No. 1.4;
RESULT 809
ID ADA98171 standard; protein; 359 AA.
DE Human secreted protein sequence #12.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 810
ID ADA44024 standard; protein; 359 AA.
DE Human secreted protein SEQ ID 212.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 6; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 811
ID ADC20341 standard; protein; 359 AA.
DE Human secreted protein - amino acid sequence #17.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 812
ID ADF10683 standard; protein; 359 AA.

DE Human secreted protein #5.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 85.5; DB 7; Length 359;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 813
ID AAB75546 standard; protein; 360 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:100.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.1%; Score 85.5; DB 4; Length 360;
Best Local Similarity 23.0%; Pred. No. 1.5;
RESULT 814
ID AAW61371 standard; protein; 439 AA.
DE Non-adrenergic SM binding protein.
PN EP848059-A1.
PD 17-JUN-1998.
PA (VETI-) VETIGEN.
Query Match 6.1%; Score 85.5; DB 2; Length 439;
Best Local Similarity 23.0%; Pred. No. 2;
RESULT 815
ID AAB75598 standard; protein; 530 AA.
DE Human secreted protein sequence encoded by gene 41 SEQ ID NO:152.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 6.1%; Score 85.5; DB 4; Length 530;
Best Local Similarity 23.0%; Pred. No. 2.6;
RESULT 816
ID AAY94910 standard; protein; 545 AA.
DE Human secreted protein clone pk366_7 protein sequence SEQ ID NO:26.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 6.1%; Score 85.5; DB 3; Length 545;
Best Local Similarity 23.0%; Pred. No. 2.7;
RESULT 817
ID AAB94667 standard; protein; 545 AA.
DE Human protein sequence SEQ ID NO:15600.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.1%; Score 85.5; DB 4; Length 545;
Best Local Similarity 23.0%; Pred. No. 2.7;
RESULT 818
ID AAY82460 standard; protein; 579 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:4.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 579;
Best Local Similarity 23.0%; Pred. No. 3;
RESULT 819
ID AAY82459 standard; protein; 582 AA.
DE Human SM-11044-binding receptor protein SEQ ID NO:2.
PN WO200014266-A1.
PD 16-MAR-2000.
PA (SUMU) SUMITOMO PHARM CO LTD.
Query Match 6.1%; Score 85.5; DB 3; Length 582;
Best Local Similarity 23.0%; Pred. No. 3;
RESULT 820
ID ABB69104 standard; protein; 700 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34104.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 85.5; DB 4; Length 700;
Best Local Similarity 19.7%; Pred. No. 3.8;
RESULT 821

ID ABU34786 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #20313.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.6;
RESULT 822
ID ABU36544 standard; protein; 338 AA.
DE Protein encoded by Prokaryotic essential gene #22071.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 85; DB 6; Length 338;
Best Local Similarity 23.1%; Pred. No. 1.6;
RESULT 823
ID AAG90802 standard; protein; 419 AA.
DE C glutamicum protein fragment SEQ ID NO: 4556.
PN EP1108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 6.1%; Score 85; DB 4; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.2;
RESULT 824
ID AAE20418 standard; protein; 419 AA.
DE Corynebacterium glutamicum CHRS protein.
PN WO200220572-A2.
PD 14-MAR-2002.
PA (DEGS) DEGUSSA AG.
Query Match 6.1%; Score 85; DB 5; Length 419;
Best Local Similarity 24.1%; Pred. No. 2.2;
RESULT 825
ID ABB55143 standard; protein; 443 AA.
DE Lactococcus lactis protein ysfC.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 85; DB 5; Length 443;
Best Local Similarity 24.4%; Pred. No. 2.3;
RESULT 826
ID AAU78998 standard; protein; 498 AA.
DE Mouse Rh type C gene (RHCG) protein.
PN WO200220719-A2.
PD 14-MAR-2002.
PA (NYBL-) NEW YORK BLOOD CENT INC.
Query Match 6.1%; Score 85; DB 5; Length 498;
Best Local Similarity 20.2%; Pred. No. 2.7;
RESULT 827
ID ADE56874 standard; protein; 1166 AA.
DE Rat Protein Q03343, SEQ ID NO 2729.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 85; DB 7; Length 1166;
Best Local Similarity 19.8%; Pred. No. 8.8;
RESULT 828
ID AAB02010 standard; protein; 1180 AA.
DE Type VI adenylyl cyclase.
PN US6107076-A.
PD 22-AUG-2000.
PA (TEXA) UNIV TEXAS SYSTEM.
Query Match 6.1%; Score 85; DB 3; Length 1180;
Best Local Similarity 19.8%; Pred. No. 9;
RESULT 829
ID ADH88320 standard; protein; 296 AA.
DE Enterococcus faecalis polypeptide #2800.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 84.5; DB 7; Length 296;
Best Local Similarity 25.2%; Pred. No. 1.5;

RESULT 830
ID ABM68417 standard; protein; 324 AA.
DE Photorhabdus luminescens protein sequence #1514.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 6.1%; Score 84.5; DB 6; Length 324;
Best Local Similarity 23.8%; Pred. No. 1.7;
RESULT 831
ID AAY07771 standard; protein; 356 AA.
DE Human secreted protein fragment encoded from gene 28.
PN WO9909155-A1.
PD 25-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 2; Length 356;
Best Local Similarity 19.8%; Pred. No. 2;
RESULT 832
ID ABG75197 standard; protein; 408 AA.
DE Wheat homogentisate geranylgeranyl transferase.
PN WO2003082899-A2.
PD 09-OCT-2003.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 6.1%; Score 84.5; DB 7; Length 408;
Best Local Similarity 25.3%; Pred. No. 2.4;
RESULT 833
ID AAG46717 standard; protein; 446 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58803.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 446;
Best Local Similarity 19.0%; Pred. No. 2.7;
RESULT 834
ID AAY95015 standard; protein; 453 AA.
DE Human secreted protein vc61_1, SEQ ID NO:70.
PN WO200011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 6.1%; Score 84.5; DB 3; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 835
ID AAG65236 standard; protein; 453 AA.
DE Protein tyrosine kinase 50.
PN CN1298944-A.
PD 13-JUN-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 836
ID AAU29065 standard; protein; 453 AA.
DE Human PRO polypeptide sequence #42.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 837
ID AAM39489 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2634.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 838
ID AAB65170 standard; protein; 453 AA.
DE Human PRO732 (UNQ396) protein sequence SEQ ID NO:73.
PN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 4; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 839

ID ABB90299 standard; protein; 453 AA.
DE Human polypeptide SEQ ID NO 2675.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.1%; Score 84.5; DB 5; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 840
ID ABU58441 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 841
ID ABU87989 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 842
ID ABU84304 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 843
ID ABR66178 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 844
ID ABR65568 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 845
ID ABU99508 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 846
ID ABU57985 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 847
ID ABU59063 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO732.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 848
ID ABU82575 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003032023-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 849
ID ABU82747 standard; protein; 453 AA.

DE Human PRO polypeptide #42.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 850
ID ABU89868 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 851
ID ABR68117 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 852
ID ABU60494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 853
ID ABU96170 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 854
ID ABU92601 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 855
ID ABO08678 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 856
ID ABO02730 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 857
ID ABR74884 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 858
ID ABR94646 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 859
ID ABU13876 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002103125-A1.

PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 860
ID ABU85619 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 861
ID ABU98779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 862
ID ABU97994 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 863
ID ABU91700 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 864
ID ABU89393 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 865
ID ABU86234 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 866
ID ABU67447 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 867
ID ABU80475 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 868
ID ABU72461 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 869

ID ABR99393 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 870
ID ABR98783 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 871
ID ABO16306 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 872
ID ABR92206 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 873
ID ABO18847 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 874
ID ABR78268 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 875
ID ABU85004 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 876
ID ABO00143 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 877
ID ABO11475 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 878
ID ABO02120 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 879
ID ABU88694 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.

PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 880
ID ABU83389 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 881
ID ABO06190 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 882
ID ABR59226 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 883
ID ABO09288 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 884
ID ABO19152 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 885
ID ABO11170 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 886
ID ABR66788 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 887
ID ABO16001 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 888
ID ABO13707 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 889
ID ABU65610 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, SEQ ID 84.
PN US2003036156-A1.
PD 20-FEB-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 890
ID ABO07458 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 891
ID ABO03645 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 892
ID ABR67093 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 893
ID ABO15696 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 894
ID ABU55977 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 895
ID ABU65305 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 896
ID ABU95250 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 897
ID ABU71153 standard; protein; 453 AA.
DE Human PRO732 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 898
ID ABO07763 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 899
ID ABR70004 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 900
ID ABR69337 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 901
ID ABO01478 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 902
ID ABU81280 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 903
ID ABR60077 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 904
ID ABR67812 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 905
ID ABR65200 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 906
ID ABR68422 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 907
ID ABR71834 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 908
ID ABU59210 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2003027162-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 909
ID ABU85314 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;

RESULT 910
ID ABU89004 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 911
ID ABU83084 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 912
ID ABU94940 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 913
ID ABU90488 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 914
ID ABU83999 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 915
ID ABU93650 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 916
ID ABO25907 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 917
ID ABR64895 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 918
ID ABR68727 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 919
ID ABO06543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 920
ID ABO22295 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

ID ABR99088 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 921
ID ABU56972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 922
ID ABU85924 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 923
ID ABU82211 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 924
ID ABU87222 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 925
ID ABU83694 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 926
ID ABO08068 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 927
ID ABU81779 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 928
ID ABU65943 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 929
ID ABR59772 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 930
ID ABU93960 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036155-A1.

PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 931
ID ABU99813 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 932
ID ABR66483 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 933
ID ABR90901 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 934
ID ABU58916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, #24.
PN US2002142961-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 935
ID ABU94328 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 936
ID ABU79210 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 937
ID ABU86539 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 938
ID ABU86844 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 939
ID ABU94633 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 940
ID ABO04560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032107-A1.
PD 13-FEB-2003.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 941
ID ABR70309 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 942
ID ABU92294 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003022187-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 943
ID ABU98474 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 944
ID ABR65873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 945
ID ABR64590 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 946
ID ABU59359 standard; protein; 453 AA.
DE Novel human secreted or transmembrane protein PRO1120.
PN US2003027985-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 947
ID ABU79515 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 948
ID ABU92906 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 949
ID ABU95865 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 950
ID ABU91085 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

RESULT 951
ID ABU90178 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 952
ID ABO09593 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 953
ID ABO10865 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 954
ID ABR70919 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 955
ID ABU87527 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 956
ID ABU91395 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 957
ID ABU84609 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 958
ID ABR69699 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 959
ID ABU80076 standard; protein; 453 AA.
DE Human PRO protein #42.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 960
ID ABU92125 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003017476-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 961
ID ABU93345 standard; protein; 453 AA.
DE Human PRO polypeptide #42.

PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 962
ID ABO09898 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 963
ID ABO08983 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 964
ID ABU10831 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 965
ID ABU10551 standard; protein; 453 AA.
DE Human secreted/transmembrane protein #42.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 966
ID ABU81583 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002177164-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 967
ID ABU95560 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 968
ID ABU96769 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 969
ID ABR70614 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 970
ID ABO04965 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 971

ID ABO08373 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 972
ID ABU88522 standard; protein; 453 AA.
DE Human secreted and transmembrane polypeptide PRO732.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 973
ID ABO34036 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 974
ID ABO05580 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 975
ID ABR73969 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 976
ID ABR95561 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 977
ID ABR80858 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 978
ID ABR81163 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 979
ID ABM00859 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 980
ID ABR88461 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 981
ID ABM77282 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 982
ID ABO28766 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 983
ID ABO31511 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 984
ID ABM07928 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 985
ID ABO40408 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 986
ID ABO35833 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 987
ID ABO43972 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 988
ID ADA77836 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 989
ID ABM24767 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

RESULT 990
ID ABO03035 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 991
ID ABR90291 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 992
ID ABM17205 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 993
ID ABR94951 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 994
ID ABR95256 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 995
ID ABO21494 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 996
ID ABR97758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 997
ID ABR87546 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 998
ID ABM77587 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 999
ID ABM27817 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064440-A1.

PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1000
ID ABM06098 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1001
ID ABM03604 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1002
ID ABM35055 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1003
ID ABM26292 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1004
ID ABO48074 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1005
ID ABR92816 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1006
ID ABO24577 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1007
ID ADA37584 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1008
ID ABM11588 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1009
ID ABM02689 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1010
ID ABM15985 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1011
ID ABO27546 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1012
ID ABM29037 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1013
ID ABM07013 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1014
ID ABM21107 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1015
ID ABM09453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1016
ID ABO41323 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1017
ID ABO36138 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1018
ID ABO43667 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1019
ID ABM76367 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082717-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1020
ID ABM76063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1021
ID ABM25682 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1022
ID ABM25987 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1023
ID ADA21270 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1024
ID ABO03340 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1025
ID ABO02425 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1026
ID ABR90596 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1027
ID ABR73664 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;

Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1028
ID ABO16916 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1029
ID ABR94341 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1030
ID ABR75848 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1031
ID ABR71224 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1032
ID ABR93121 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1033
ID ABR93426 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1034
ID ADA10057 standard; protein; 453 AA.
DE Human secreted/transmembrane protein, PRO732.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1035
ID ABR87851 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1036
ID ABO27851 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1037
ID ABO29986 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.

PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1038
ID ABO33195 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1039
ID ABM04883 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1040
ID ABM08843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1041
ID ABO36443 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1042
ID ABO35528 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1043
ID ABO39493 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1044
ID ABM10368 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1045
ID ABM11893 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1046
ID ABO52039 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049768-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1047
ID ABO52344 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1048
ID ABO23662 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1049
ID ADA17601 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1050
ID ABR97148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1051
ID ABR86936 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1052
ID ABM10978 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1053
ID ABM28122 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1054
ID ABO32121 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1055
ID ABM15248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1056
ID ABM06403 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1057
ID ABM04214 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1058
ID ABM22327 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1059
ID ABM07623 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1060
ID ABO40713 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1061
ID ABM35360 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1062
ID ABM33123 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1063
ID ABO52649 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1064
ID ABO50209 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1065
ID ABO50209 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

ID ABU99203 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1066
ID ABO04255 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1067
ID ABO05885 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1068
ID ABM18425 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1069
ID ADA27709 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1070
ID ABR97453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1071
ID ABR80553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1072
ID ABM01164 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1073
ID ABR88766 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1074
ID ABM13418 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1075
ID ABM20802 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1076
ID ABO41933 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1077
ID ABO42543 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1078
ID ABM10063 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1079
ID ABO38578 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1080
ID ABM32818 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1081
ID ABM22632 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1082
ID ABM74843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1083
ID ADA79628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1084
ID ABR96233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003054458-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1085
ID ABM02384 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1086
ID ABR86326 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1087
ID ABR86631 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1088
ID ABM16595 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1089
ID ABM29647 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1090
ID ABO29071 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1091
ID ABM23852 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1092
ID ABM23242 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1093
ID ABM22022 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068742-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1094
ID ABO37663 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1095
ID ABM28427 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082715-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1096
ID ABM28732 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003082716-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1097
ID ABM66376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1098
ID ABM75758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1099
ID ABM34038 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1100
ID ABM34343 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1101
ID ABO20274 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1102
ID ABO21189 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1103
ID ABO22104 standard; protein; 453 AA.

DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1104
ID ABR96538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1105
ID ADA94289 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059832-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1106
ID ABR85716 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1107
ID ABR99698 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1108
ID ABM00554 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1109
ID ABM00249 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1110
ID ABO29681 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1111
ID ABM23547 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1112
ID ABM29342 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1113
ID ABO38273 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1114
ID ABO45573 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1115
ID ABM20497 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1116
ID ADA81355 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1117
ID ABO16611 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003027276-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1118
ID ABO18237 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1119
ID ABO22664 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1120
ID ABO22969 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1121
ID ABR92511 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1122
ID ABR81468 standard; protein; 453 AA.

DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1123
ID ABM77892 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1124
ID ABR89681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1125
ID ABM26597 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1126
ID ABM13723 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1127
ID ABO28461 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1128
ID ABO30291 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1129
ID ABM07318 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1130
ID ABM03909 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.1%; Score 84.5; DB 6; Length 453;
RESULT 1131
ID ABO37053 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068719-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1132
ID ABO41628 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1133
ID ABO35223 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1134
ID ABM25072 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1135
ID ABO47464 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1136
ID ABO47769 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1137
ID ABO48379 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1138
ID ABO51429 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1139
ID ABO51734 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1140
ID ABO50514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1141
ID ABR79638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1142
ID ABM16900 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1143
ID ABO17932 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1144
ID ABO20884 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1145
ID ABR96843 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1146
ID ADA38514 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1147
ID ABM12198 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1148
ID ABM16290 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1149
ID ABM24157 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1150
ID ABM14638 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068696-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1151
ID ABM04519 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1152
ID ABM06708 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1153
ID ABM09148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1154
ID ABO39188 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1155
ID ABM75453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1156
ID ABM25377 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1157
ID ABM19887 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1158
ID ABO46793 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1159
ID ABO47098 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

RESULT 1160
ID ADA83153 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1161
ID ABR71529 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1162
ID ABR72139 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1163
ID ABR98478 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1164
ID ABO06848 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1165
ID ABR84801 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1166
ID ABR73359 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1167
ID ABR76453 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1168
ID ABR73054 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1169
ID ABM18120 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

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RESULT 1170
ID ABO20579 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1171
ID ABO25322 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1172
ID ABO25627 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1173
ID ABR94036 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1174
ID ADA92635 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1175
ID ABR79943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1176
ID ABM11283 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1177
ID ABO32890 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1178
ID ABO30596 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1179
ID ABO30901 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064468-A1.
PD 10-APR-2003.
PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1180
ID ABM27207 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1181
ID ABM29952 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1182
ID ABM05488 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1183
ID ABM15553 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1184
ID ABM08538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1185
ID ABO42238 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1186
ID ABO37968 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1187
ID ABO45878 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1188
ID ABM66681 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068688-A1.
PD 10-APR-2003.
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PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1189
ID ADB20196 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1190
ID ABM19582 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1191
ID ABO49294 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1192
ID ABO49599 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1193
ID ADA78448 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1194
ID ABR88156 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1195
ID ABM26902 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1196
ID ABM03299 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1197
ID ABO39798 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 6; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1198
ID ABO49904 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1199
ID ABO50819 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1200
ID ABO05275 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1201
ID ABR74579 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1202
ID ABR77058 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1203
ID ABM17815 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1204
ID ABR95866 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1205
ID ABO21799 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1206
ID ABO19969 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1207
ID ABO24272 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1208
ID ABR86021 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1209
ID ABM10673 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1210
ID ABM76672 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1211
ID ABR89376 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1212
ID ABM12503 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1213
ID ABM05793 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1214
ID ABO34918 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1215
ID ABM02994 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1216
ID ABM18972 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

RESULT 1217
ID ABM19277 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1218
ID ABO46488 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1219
ID ABO48989 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1220
ID ABR69032 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003027273-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1221
ID ABR89071 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036119-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1222
ID ABR72444 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036120-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1223
ID ABR74274 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1224
ID ABO18542 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044921-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1225
ID ABR80248 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1226
ID ABM01469 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059882-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1227
ID ABM02079 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1228
ID ABR87241 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1229
ID ABM12808 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1230
ID ABM30562 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1231
ID ABM24462 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1232
ID ABO29376 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1233
ID ABO31206 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1234
ID ABM14333 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1235
ID ABM09758 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1236
ID ABO38883 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1237
ID ABM34648 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1238
ID ABO51124 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1239
ID ABO03950 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1240
ID ABO10420 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1241
ID ABO53122 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1242
ID ABR77663 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1243
ID ABR78873 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1244
ID ABO23967 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1245
ID ABR93731 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054457-A1.
PD 20-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1246
ID ABM01774 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1247
ID ABM78197 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1248
ID ABR89986 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1249
ID ADA22196 standard; protein; 453 AA.
DE Human secreted/transmembrane polypeptide PRO732.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1250
ID ABM27512 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1251
ID ABM13113 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1252
ID ABO31816 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1253
ID ABM14028 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1254
ID ABM08233 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

RESULT 1255
ID ABO40103 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1256
ID ABM74538 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1257
ID ABM33733 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1258
ID ABM20192 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1259
ID ABO48684 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1260
ID ABO22492 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1261
ID ABR72749 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1262
ID ABO15391 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1263
ID ABR85106 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1264
ID ABO15086 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003044919-A1.
PD 06-MAR-2003.

Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1265
ID ABO17221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1266
ID ABM17510 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1267
ID ADA06362 standard; protein; 453 AA.
DE Human secreted/transmembrane PRO polypeptide #17.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1268
ID ADA39055 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1269
ID ABR85411 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1270
ID ABM76977 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1271
ID ABO28156 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1272
ID ABM22937 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1273
ID ABM30257 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1274
ID ABM21717 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.

PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1275
ID ABM21412 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1276
ID ABM14943 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1277
ID ABO41018 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1278
ID ABO36748 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1279
ID ABO37358 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1280
ID ABM75148 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1281
ID ABM33428 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1282
ID ABO46183 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1283
ID ADA82519 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003049755-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1284
ID ADB96081 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003054403-A1.
PD 20-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1285
ID ABM31782 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1286
ID ABM31172 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1287
ID ADB85827 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1288
ID ABM32087 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1289
ID ABM32392 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1290
ID ABM31477 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1291
ID ABM30867 standard; protein; 453 AA.
DE Human secreted polypeptide PRO732, SEQ ID NO:84.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1292
ID ADC57553 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003027754-A1.
PD 06-FEB-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;

RESULT 1293
ID ADC54917 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003045463-A1.
PD 06-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1294
ID ADC11784 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003049681-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1295
ID ADC56206 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003064375-A1.
PD 03-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1296
ID ADC07261 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003068647-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1297
ID ADC11251 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003069403-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1298
ID ADC14373 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1299
ID ADD07905 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1300
ID ADC81730 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1301
ID ADD07372 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1302
ID ADC77580 standard; protein; 453 AA.
DE Human TMS2 amino acid sequence.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1303

ID ADC82263 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1304
ID ADD05557 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1305
ID ADD08443 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1306
ID ADD06692 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1307
ID ADC82939 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1308
ID ADD55046 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1309
ID ADD56004 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1310
ID ADD54442 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1311
ID ADE26596 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1312
ID ADE26063 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1313

ID ADF67000 standard; protein; 453 AA.
DE Human PRO732 amino acid sequence SEQ ID NO:73.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1314
ID ADG02552 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1315
ID ADG01259 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1316
ID ADF95434 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1317
ID ADG12249 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207392-A1.
PD 06-NOV-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1318
ID ADH08909 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1319
ID ADI35254 standard; protein; 453 AA.
DE Human PRO polypeptide #17.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1320
ID ADH99746 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003049682-A1.
PD 13-MAR-2003.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1321
ID ADL32690 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1322
ID ADM30224 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003073813-A1.
PD 17-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 7; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1323
ID ADE74221 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211572-A1.
PD 13-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1324
ID ADE74833 standard; protein; 453 AA.
DE Human secreted/transmembrane protein (PRO) #42.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1325
ID ADF35199 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1326
ID ADG11449 standard; protein; 453 AA.
DE Human PRO732 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1327
ID ADF96046 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1328
ID ADG04317 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1329
ID ADG00477 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1330
ID ADG82733 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1331
ID ADH26014 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1332
ID ADH19319 standard; protein; 453 AA.

DE Human secreted/transmembrane protein PRO732.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1333
ID ADH32983 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1334
ID ADH20812 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1335
ID ADH19852 standard; protein; 453 AA.
DE Human secreted/transmembrane protein PRO732.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1336
ID ADJ54722 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004023321-A1.
PD 05-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1337
ID ADJ64493 standard; protein; 453 AA.
DE Human PRO polypeptide #42.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1338
ID ADM31389 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1339
ID ADM36436 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1340
ID ADM40241 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1341
ID ADN37849 standard; protein; 453 AA.
DE Novel human secreted and transmembrane protein PRO732.
PN US2004091959-A1.

PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1342
ID ADR09184 standard; protein; 453 AA.
DE Human protein useful for treating neurological disease Seq 2690.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1343
ID ABM80816 standard; protein; 453 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO81457, SEQ:2102.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1344
ID ADR99176 standard; protein; 453 AA.
DE KIAA1253, SEQ ID 182.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 6.1%; Score 84.5; DB 8; Length 453;
Best Local Similarity 19.8%; Pred. No. 2.7;
RESULT 1345
ID ADG10618 standard; protein; 472 AA.
DE Human STAT6-activating protein, SEQ ID NO:208.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAHI KASEI KOGYO KK.
Query Match 6.1%; Score 84.5; DB 7; Length 472;
Best Local Similarity 19.8%; Pred. No. 2.9;
RESULT 1346
ID AAM41275 standard; protein; 477 AA.
DE Human polypeptide SEQ ID NO 6206.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 84.5; DB 4; Length 477;
Best Local Similarity 19.8%; Pred. No. 2.9;
RESULT 1347
ID AAG46716 standard; protein; 521 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58802.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 521;
Best Local Similarity 19.0%; Pred. No. 3.3;
RESULT 1348
ID ABB93783 standard; protein; 562 AA.
DE Herbicidally active polypeptide SEQ ID NO 2994.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 84.5; DB 5; Length 562;
Best Local Similarity 19.6%; Pred. No. 3.7;
RESULT 1349
ID AAG46715 standard; protein; 571 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 58801.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.1%; Score 84.5; DB 3; Length 571;
Best Local Similarity 19.0%; Pred. No. 3.8;
RESULT 1350
ID ADA36714 standard; protein; 241 AA.
DE Acinetobacter baumannii protein #3875.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 6; Length 241;

Best Local Similarity 22.8%; Pred. No. 1.3;
RESULT 1351
ID ABG61495 standard; protein; 318 AA.
DE Iron uptake ABC transporter polypeptide #2.
PN WO200234773-A2.
PD 02-MAY-2002.
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
Query Match 6.0%; Score 84; DB 5; Length 318;
Best Local Similarity 24.4%; Pred. No. 1.9;
RESULT 1352
ID ABU02362 standard; protein; 318 AA.
DE S. pneumoniae type 4 strain protein from coding region #1940.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.0%; Score 84; DB 6; Length 318;
Best Local Similarity 24.4%; Pred. No. 1.9;
RESULT 1353
ID ABG10541 standard; protein; 480 AA.
DE Novel human diagnostic protein #10532.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 84; DB 4; Length 480;
Best Local Similarity 20.5%; Pred. No. 3.4;
RESULT 1354
ID ADL04919 standard; protein; 506 AA.
DE M. catarrhalis protein #685.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 8; Length 506;
Best Local Similarity 19.9%; Pred. No. 3.6;
RESULT 1355
ID ADS23392 standard; protein; 516 AA.
DE Bacterial polypeptide #12425.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.0%; Score 84; DB 8; Length 516;
Best Local Similarity 25.0%; Pred. No. 3.7;
RESULT 1356
ID ABO67632 standard; protein; 537 AA.
DE Klebsiella pneumoniae polypeptide seqid 14149.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 537;
Best Local Similarity 18.7%; Pred. No. 3.9;
RESULT 1357
ID ABU38257 standard; protein; 575 AA.
DE Protein encoded by Prokaryotic essential gene #23784.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 84; DB 6; Length 575;
Best Local Similarity 20.3%; Pred. No. 4.3;
RESULT 1358
ID ABO73781 standard; protein; 602 AA.
DE Pseudomonas aeruginosa polypeptide #5956.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 602;
Best Local Similarity 20.3%; Pred. No. 4.6;
RESULT 1359
ID ABO70835 standard; protein; 720 AA.
DE Pseudomonas aeruginosa polypeptide #3010.

PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 720;
Best Local Similarity 21.8%; Pred. No. 5.9;
RESULT 1360
ID ABU32051 standard; protein; 1137 AA.
DE Protein encoded by Prokaryotic essential gene #17578.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 84; DB 6; Length 1137;
Best Local Similarity 18.6%; Pred. No. 11;
RESULT 1361
ID ABO67057 standard; protein; 1138 AA.
DE Klebsiella pneumoniae polypeptide seqid 13574.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 84; DB 7; Length 1138;
Best Local Similarity 18.6%; Pred. No. 11;
RESULT 1362
ID ABU37874 standard; protein; 295 AA.
DE Protein encoded by Prokaryotic essential gene #23401.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83.5; DB 6; Length 295;
Best Local Similarity 21.6%; Pred. No. 2;
RESULT 1363
ID AAR97984 standard; protein; 618 AA.
DE DmORF1 potassium channel protein.
PN WO9613520-A1.
PD 09-MAY-1996.
PA (AMCY) AMERICAN CYANAMID CO.
Query Match 6.0%; Score 83.5; DB 2; Length 618;
Best Local Similarity 19.9%; Pred. No. 5.4;
RESULT 1364
ID AAU07616 standard; protein; 618 AA.
DE Drosophila melanogaster potassium ion channel ORF1 (DmORF1) protein.
PN WO200161006-A2.
PD 23-AUG-2001.
PA (BADI) BASF CORP.
Query Match 6.0%; Score 83.5; DB 4; Length 618;
Best Local Similarity 19.9%; Pred. No. 5.4;
RESULT 1365
ID ABC30123 standard; protein; 1027 AA.
DE Novel human diagnostic protein #30114.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.0%; Score 83.5; DB 4; Length 1027;
Best Local Similarity 19.8%; Pred. No. 11;
RESULT 1366
ID ABU28293 standard; protein; 1090 AA.
DE Protein encoded by Prokaryotic essential gene #13820.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83.5; DB 6; Length 1090;
Best Local Similarity 18.5%; Pred. No. 12;
RESULT 1367
ID AAG44538 standard; protein; 250 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55802.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 83; DB 3; Length 250;
Best Local Similarity 21.7%; Pred. No. 1.8;
RESULT 1368
ID AAG66371 standard; protein; 305 AA.
DE Human partial olfactory receptor-like protein OLF3 #2.
PN WO200155179-A2.
PD 02-AUG-2001.

PA (CURA-) CURAGEN CORP.
Query Match 6.0%; Score 83; DB 4; Length 305;
Best Local Similarity 20.6%; Pred. No. 2.3;
RESULT 1369
ID AAY85935 standard; protein; 318 AA.
DE S. pneumoniae derived protein #144.
PN WO9806734-A1.
PD 19-FEB-1998.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 6.0%; Score 83; DB 2; Length 318;
Best Local Similarity 24.4%; Pred. No. 2.5;
RESULT 1370
ID ADK46461 standard; protein; 318 AA.
DE Streptococcus pneumoniae protein, Seq ID No 2976.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 8; Length 318;
Best Local Similarity 24.4%; Pred. No. 2.5;
RESULT 1371
ID AAG71916 standard; protein; 319 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1597.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 6.0%; Score 83; DB 4; Length 319;
Best Local Similarity 20.6%; Pred. No. 2.5;
RESULT 1372
ID AAB46999 standard; protein; 321 AA.
DE Human OLFXY protein.
PN DE19937839-A1.
PD 15-FEB-2001.
PA (BRUE/) BRUESS M.
PA (BOEN/) BOENISCH H.
Query Match 6.0%; Score 83; DB 4; Length 321;
Best Local Similarity 20.6%; Pred. No. 2.5;
RESULT 1373
ID ABP95927 standard; protein; 321 AA.
DE Human GPCR polypeptide SEQ ID NO 664.
PN WO200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.0%; Score 83; DB 5; Length 321;
Best Local Similarity 20.6%; Pred. No. 2.5;
RESULT 1374
ID ADR96441 standard; protein; 336 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 5076.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 8; Length 336;
Best Local Similarity 24.4%; Pred. No. 2.7;
RESULT 1375
ID ABU43979 standard; protein; 355 AA.
DE Protein encoded by Prokaryotic essential gene #29506.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 83; DB 6; Length 355;
Best Local Similarity 23.0%; Pred. No. 2.9;
RESULT 1376
ID ABO62213 standard; protein; 417 AA.
DE Klebsiella pneumoniae polypeptide seqid 8730.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.0%; Score 83; DB 7; Length 417;
Best Local Similarity 20.8%; Pred. No. 3.6;
RESULT 1377
ID AAY66647 standard; protein; 455 AA.
DE Membrane-bound protein PRO732.
PN WO9963088-A2.

PD 09-DEC-1999.
PA (GETH) GENENTECH INC. 6.0%; Score 83; DB 3; Length 455;
Query Match
Best Local Similarity 19.8%; Pred. No. 4.1;
RESULT 1378
ID AAB96670 standard; protein; 490 AA.
DE Putative P. abyssi succinyl-CoA synthetase #5.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match
Best Local Similarity 23.6%; Pred. No. 4.5;
RESULT 1379
ID ABO70524 standard; protein; 542 AA.
DE Pseudomonas aeruginosa polypeptide #2699.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 20.2%; Pred. No. 5.2;
RESULT 1380
ID ADA33498 standard; protein; 632 AA.
DE Acinetobacter baumannii protein #659.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 25.1%; Pred. No. 6.4;
RESULT 1381
ID ABB65640 standard; protein; 774 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 23712.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 22.4%; Pred. No. 8.5;
RESULT 1382
ID AAU38963 standard; protein; 774 AA.
DE Drosophila G-protein coupled receptor, GCPR #41.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 22.4%; Pred. No. 8.5;
RESULT 1383
ID ADC35871 standard; protein; 774 AA.
DE Drosophila G protein coupled receptor seq id 43.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 22.4%; Pred. No. 8.5;
RESULT 1384
ID AAE38199 standard; protein; 802 AA.
DE Fruit fly G protein-coupled receptor (GPCR) protein #48.
PN WO2003052078-A2.
PD 26-JUN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match
Best Local Similarity 22.4%; Pred. No. 8.9;
RESULT 1385
ID ABP70924 standard; protein; 2159 AA.
DE Maize DEK1 from B73.
PN WO2003011015-A2.
PD 13-FEB-2003.
PA (PION-) PIONEER HI-BRED INT INC.
Query Match
Best Local Similarity 20.6%; Pred. No. 35;
RESULT 1386
ID ADS43623 standard; protein; 391 AA.
DE Bacterial polypeptide #22053.
PN US2003233675-A1.

PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 23.2%; Pred. No. 3.8;
RESULT 1387
ID ABU28011 standard; protein; 395 AA.
DE Protein encoded by Prokaryotic essential gene #13538.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 19.7%; Pred. No. 3.8;
RESULT 1388
ID AAW21009 standard; protein; 461 AA.
DE H. pylori cell envelope transporter protein, hp5e11726orf7.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match
Best Local Similarity 21.5%; Pred. No. 4.7;
RESULT 1389
ID ABO69393 standard; protein; 492 AA.
DE Pseudomonas aeruginosa polypeptide #1568.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 19.1%; Pred. No. 5.2;
RESULT 1390
ID ADN18812 standard; protein; 596 AA.
DE Bacterial polypeptide #1465.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 20.6%; Pred. No. 6.7;
RESULT 1391
ID ABG06558 standard; protein; 875 AA.
DE Novel human diagnostic protein #6549.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 26.0%; Pred. No. 11;
RESULT 1392
ID ADJ69204 standard; protein; 1457 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1010.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 26.0%; Pred. No. 23;
RESULT 1393
ID ADJ69205 standard; protein; 1457 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1011.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 26.0%; Pred. No. 23;
RESULT 1394
ID ADJ58460 standard; protein; 1457 AA.
DE BAB13458.1(P450G5) protein.

PN WO2004011648-A2.
PD 05-FEB-2004.
PA (INPH-) INPHARMATICA LTD.
Query Match 5.9%; Score 82.5; DB 8; Length 1457;
Best Local Similarity 26.0%; Pred. No. 23;
RESULT 1395
ID ADC31246 standard; protein; 2548 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1328.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 82.5; DB 7; Length 2548;
Best Local Similarity 26.0%; Pred. No. 50;
RESULT 1396
ID ABO84919 standard; protein; 219 AA.
DE Human cancer-associated protein (CAP) HP07-069.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.9%; Score 82; DB 8; Length 219;
Best Local Similarity 22.1%; Pred. No. 1.9;
RESULT 1397
ID AAB87783 standard; protein; 299 AA.
DE Rat T2R03 amino acid sequence SEQ ID NO:81.
PN WO200118050-A2.
PD 15-MAR-2001.
PA (REGC) UNIV CALIFORNIA.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.9%; Score 82; DB 4; Length 299;
Best Local Similarity 22.8%; Pred. No. 3;
RESULT 1398
ID ADJ84452 standard; protein; 299 AA.
DE Rat T2R G-protein coupled receptor seq id 5.
PN US2004038312-A1.
PD 26-FEB-2004.
PA (ZUKE/) ZUKER C S.
PA (ADLE/) ADLER J E.
PA (HOON/) HOON M.
PA (RYBA/) RYBA N.
PA (MUEL/) MUELLER K.
Query Match 5.9%; Score 82; DB 8; Length 299;
Best Local Similarity 22.8%; Pred. No. 3;
RESULT 1399
ID ADR29142 standard; protein; 299 AA.
DE Taste receptor modulation-related rat T2R03 protein sequence SeqID81.
PN WO2004069191-A2.
PD 19-AUG-2004.
PA (SENO-) SENOMYX INC.
Query Match 5.9%; Score 82; DB 8; Length 299;
Best Local Similarity 22.8%; Pred. No. 3;
RESULT 1400
ID AAB10684 standard; protein; 356 AA.
DE A. thaliana PUP1 protein.
PN DE19907209-A1.
PD 24-AUG-2000.
PA (FROM/) FROMMER W.
Query Match 5.9%; Score 82; DB 3; Length 356;
Best Local Similarity 19.4%; Pred. No. 3.8;
RESULT 1401
ID ABB91157 standard; protein; 356 AA.
DE Herbicidally active polypeptide SEQ ID NO 368.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 82; DB 5; Length 356;
Best Local Similarity 19.4%; Pred. No. 3.8;
RESULT 1402
ID ABU28157 standard; protein; 417 AA.
DE Protein encoded by Prokaryotic essential gene #13684.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 82; DB 6; Length 417;

Best Local Similarity 27.1%; Pred. No. 4.7;
RESULT 1403
ID ADK16901 standard; protein; 465 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #426.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.9%; Score 82; DB 8; Length 465;
Best Local Similarity 23.7%; Pred. No. 5.5;
RESULT 1404
ID ABO81608 standard; protein; 474 AA.
DE Pseudomonas aeruginosa polypeptide #13783.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 82; DB 7; Length 474;
Best Local Similarity 20.1%; Pred. No. 5.6;
RESULT 1405
ID ADN23219 standard; protein; 573 AA.
DE Bacterial polypeptide #5872.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82; DB 8; Length 573;
Best Local Similarity 18.5%; Pred. No. 7.3;
RESULT 1406
ID ADN23218 standard; protein; 573 AA.
DE Bacterial polypeptide #5871.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 82; DB 8; Length 573;
Best Local Similarity 18.5%; Pred. No. 7.3;
RESULT 1407
ID ABU50193 standard; protein; 1139 AA.
DE Protein encoded by Prokaryotic essential gene #35720.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 82; DB 6; Length 1139;
Best Local Similarity 19.5%; Pred. No. 19;
RESULT 1408
ID AAE04312 standard; protein; 1167 AA.
DE Human modified cardiac adenylylase VI (ACVI) isoform.
PN WO200148164-A2.
PD 05-JUL-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.9%; Score 82; DB 4; Length 1167;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1409
ID ABG32870 standard; protein; 1167 AA.
DE Chimaeric Adenylylase isoform 6, AC-VI.
PN US2002103147-A1.
PD 01-AUG-2002.
PA (HAMM/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
Query Match 5.9%; Score 82; DB 5; Length 1167;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1410
ID AAW30599 standard; protein; 1168 AA.
DE Human type VI adenylyl cyclase.
PN WO9901547-A1.

PD 14-JAN-1999.
PA (CORT-) COR THERAPEUTICS INC.
Query Match 5.9%; Score 82; DB 2; Length 1168;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1411
ID AAE04311 standard; protein; 1168 AA.
DE Human cardiac adenylcyclase VI (ACVI) isoform #2.
PN WO200148164-A2.
PD 05-JUL-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.9%; Score 82; DB 4; Length 1168;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1412
ID ABG32869 standard; protein; 1168 AA.
DE Human Adenylcyclase isoform 6, AC-VI, #2.
PN US2002103147-A1.
PD 01-AUG-2002.
PA (HAMM/) HAMMOND H K.
PA (INSE/) INSEL P A.
PA (PING/) PING P.
PA (POST/) POST S R.
PA (GAOM/) GAO M.
Query Match 5.9%; Score 82; DB 5; Length 1168;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1413
ID ADE56876 standard; protein; 1168 AA.
DE Human Protein O43306, SEQ ID NO 2731.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 82; DB 7; Length 1168;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1414
ID ADQ89850 standard; protein; 1168 AA.
DE Antagonist of cell cycle progression polypeptide #140.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 5.9%; Score 82; DB 8; Length 1168;
Best Local Similarity 20.2%; Pred. No. 19;
RESULT 1415
ID ADK46612 standard; protein; 199 AA.
DE Streptococcus pneumoniae protein, Seq ID No 3127.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 8; Length 199;
Best Local Similarity 20.2%; Pred. No. 1.9;
RESULT 1416
ID ABU02196 standard; protein; 205 AA.
DE S. pneumoniae type 4 strain protein from coding region #1774.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.9%; Score 81.5; DB 6; Length 205;
Best Local Similarity 20.2%; Pred. No. 2;
RESULT 1417
ID AAY81546 standard; protein; 206 AA.
DE Streptococcus pneumoniae type 4 protein sequence #46.
PN WO200006737-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNICS LTD.
Query Match 5.9%; Score 81.5; DB 3; Length 206;
Best Local Similarity 20.2%; Pred. No. 2;
RESULT 1418
ID ADR96056 standard; protein; 208 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4691.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 8; Length 208;

Best Local Similarity 20.2%; Pred. No. 2.1;
RESULT 1419
ID ABU41035 standard; protein; 278 AA.
DE Protein encoded by Prokaryotic essential gene #26562.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 6; Length 278;
Best Local Similarity 21.0%; Pred. No. 3.1;
RESULT 1420
ID ADF05890 standard; protein; 280 AA.
DE Bacterial polypeptide #2003.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 7; Length 280;
Best Local Similarity 21.0%; Pred. No. 3.1;
RESULT 1421
ID ABB91156 standard; protein; 351 AA.
DE Herbicidally active polypeptide SEQ ID NO 367.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 81.5; DB 5; Length 351;
Best Local Similarity 23.1%; Pred. No. 4.2;
RESULT 1422
ID AAM93355 standard; protein; 399 AA.
DE Human polypeptide, SEQ ID NO: 2909.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 5.9%; Score 81.5; DB 4; Length 399;
Best Local Similarity 22.6%; Pred. No. 5;
RESULT 1423
ID ADL30876 standard; protein; 399 AA.
DE Human protein encoded by a full length cDNA clone SeqID 2909.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 81.5; DB 8; Length 399;
Best Local Similarity 22.6%; Pred. No. 5;
RESULT 1424
ID ABU39717 standard; protein; 425 AA.
DE Protein encoded by Prokaryotic essential gene #25244.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 6; Length 425;
Best Local Similarity 19.6%; Pred. No. 5.5;
RESULT 1425
ID AAU33707 standard; protein; 438 AA.
DE Pseudomonas aeruginosa cellular proliferation protein #151.
PN WO200170955-A2.
PD 27-SEP-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 4; Length 438;
Best Local Similarity 20.3%; Pred. No. 5.7;
RESULT 1426
ID ABU15597 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #1124.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 81.5; DB 6; Length 438;
Best Local Similarity 20.3%; Pred. No. 5.7;
RESULT 1427
ID ABO83917 standard; protein; 503 AA.
DE Pseudomonas aeruginosa polypeptide #16092.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 81.5; DB 7; Length 503;
Best Local Similarity 20.3%; Pred. No. 6.9;

RESULT 1428
ID ABP65039 standard; protein; 234 AA.
DE Mouse membrane spanning 4-domain family, subfamily A 7 protein.
PN WO200262946-A2.
PD 15-AUG-2002.
PA (UYDU-) UNIV DUKE.
Query Match 5.8%; Score 81; DB 5; Length 234;
Best Local Similarity 20.6%; Pred. No. 2.8;
RESULT 1429
ID ADD43824 standard; protein; 293 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 119.
PN WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 81; DB 7; Length 293;
Best Local Similarity 18.4%; Pred. No. 3.7;
RESULT 1430
ID ADA34894 standard; protein; 323 AA.
DE Acinetobacter baumannii protein #2055.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 6; Length 323;
Best Local Similarity 22.5%; Pred. No. 4.3;
RESULT 1431
ID AAO20532 standard; protein; 392 AA.
DE Protein of the human TFM-2 gene sequence.
PN WO200229041-A2.
PD 11-APR-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 5; Length 392;
Best Local Similarity 17.8%; Pred. No. 5.6;
RESULT 1432
ID ADD37455 standard; protein; 394 AA.
DE Human transporter TFM-2.
PN US2003143675-A1.
PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 81; DB 7; Length 394;
Best Local Similarity 17.8%; Pred. No. 5.6;
RESULT 1433
ID ABO61692 standard; protein; 425 AA.
DE Klebsiella pneumoniae polypeptide seqid 8209.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 81; DB 7; Length 425;
Best Local Similarity 22.7%; Pred. No. 6.3;
RESULT 1434
ID AAE21184 standard; protein; 515 AA.
DE Human TRICH-28 protein.
PN WO200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.8%; Score 81; DB 5; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1435
ID ABJ37907 standard; protein; 515 AA.
DE NOVX protein sequence SEQ ID No 60.
PN WO200281517-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 81; DB 6; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1436
ID ADQ66916 standard; protein; 515 AA.
DE Novel human protein sequence #1889.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 81; DB 8; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1437

ID ABO84581 standard; protein; 515 AA.
DE Human cancer-associated protein HP17-001.2.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.8%; Score 81; DB 8; Length 515;
Best Local Similarity 17.8%; Pred. No. 8.1;
RESULT 1438
ID ADH58563 standard; protein; 516 AA.
DE Human Na+-independent transporter-related transporter protein.
PN WO2003076644-A2.
PD 18-SEP-2003.
PA (APPL-) APPLERA CORP.
Query Match 5.8%; Score 81; DB 7; Length 516;
Best Local Similarity 17.8%; Pred. No. 8.2;
RESULT 1439
ID ADN23220 standard; protein; 544 AA.
DE Bacterial polypeptide #5873.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 81; DB 8; Length 544;
Best Local Similarity 23.0%; Pred. No. 8.8;
RESULT 1440
ID ABB64860 standard; protein; 875 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21372.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 81; DB 4; Length 875;
Best Local Similarity 20.9%; Pred. No. 17;
RESULT 1441
ID ABU39716 standard; protein; 1102 AA.
DE Protein encoded by Prokaryotic essential gene #25243.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 81; DB 6; Length 1102;
Best Local Similarity 20.0%; Pred. No. 23;
RESULT 1442
ID ABO65403 standard; protein; 298 AA.
DE Klebsiella pneumoniae polypeptide seqid 11920.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 80.5; DB 7; Length 298;
Best Local Similarity 18.5%; Pred. No. 4.4;
RESULT 1443
ID ABB32477 standard; protein; 359 AA.
DE Staphylococcus aureus polypeptide SEQ ID NO 14.
PN WO200177365-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 80.5; DB 5; Length 359;
Best Local Similarity 23.4%; Pred. No. 5.7;
RESULT 1444
ID ABM72555 standard; protein; 359 AA.
DE Staphylococcus aureus protein #1795.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 80.5; DB 6; Length 359;
Best Local Similarity 23.4%; Pred. No. 5.7;
RESULT 1445
ID ADC21330 standard; protein; 359 AA.
DE Staphylococcus aureus protein SEQ ID NO: 12.
PN WO2003029484-A2.
PD 10-APR-2003.
PA (PHAA) PHARMACIA & UPJOHN CO.

Query Match
Best Local Similarity 5.8%; Score 80.5; DB 7; Length 359;
RESULT 1446
ID ADC25016 standard; protein; 359 AA.
DE S. aureus polypeptide #6.
PN US2003087321-A1.
PD 08-MAY-2003.
PA (TOMI/) TOMICH C C.
PA (QUIN/) QUINN C L.
PA (ARVI/) ARVIDSON S.
PA (MOTT/) MOTT J E.
PA (HARR/) HARRIS D W.
Query Match 5.8%; Score 80.5; DB 7; Length 359;
Best Local Similarity 23.4%; Pred. No. 5.7;
RESULT 1447
ID ADD52518 standard; protein; 359 AA.
DE Staphylococcus aureus unknown protein #6.
PN US2003180821-A1.
PD 25-SEP-2003.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 80.5; DB 7; Length 359;
Best Local Similarity 23.4%; Pred. No. 5.7;
RESULT 1448
ID ABB32489 standard; protein; 370 AA.
DE Staphylococcus aureus polypeptide SEQ ID NO 74.
PN WO200177365-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 80.5; DB 5; Length 370;
Best Local Similarity 23.4%; Pred. No. 5.9;
RESULT 1449
ID ADC21396 standard; protein; 370 AA.
DE Staphylococcus aureus protein SEQ ID NO: 78.
PN WO2003029484-A2.
PD 10-APR-2003.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 80.5; DB 7; Length 370;
Best Local Similarity 23.4%; Pred. No. 5.9;
RESULT 1450
ID ADC25082 standard; protein; 370 AA.
DE S. aureus polypeptide #6 encoded by the essential coding region.
PN US2003087321-A1.
PD 08-MAY-2003.
PA (TOMI/) TOMICH C C.
PA (QUIN/) QUINN C L.
PA (ARVI/) ARVIDSON S.
PA (MOTT/) MOTT J E.
PA (HARR/) HARRIS D W.
Query Match 5.8%; Score 80.5; DB 7; Length 370;
Best Local Similarity 23.4%; Pred. No. 5.9;
RESULT 1451
ID ADD52584 standard; protein; 370 AA.
DE Staphylococcus aureus essential protein #22.
PN US2003180821-A1.
PD 25-SEP-2003.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 80.5; DB 7; Length 370;
Best Local Similarity 23.4%; Pred. No. 5.9;
RESULT 1452
ID ABP38454 standard; protein; 411 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3299.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 80.5; DB 5; Length 411;
Best Local Similarity 22.0%; Pred. No. 6.8;
RESULT 1453
ID ADS07146 standard; protein; 411 AA.
DE Staphylococcus epidermis polypeptide seqid 6441.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.

Query Match
Best Local Similarity 5.8%; Score 80.5; DB 8; Length 411;
RESULT 1454
ID ABU41976 standard; protein; 438 AA.
DE Protein encoded by Prokaryotic essential gene #27503.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 80.5; DB 6; Length 438;
Best Local Similarity 18.7%; Pred. No. 7.4;
RESULT 1455
ID ADC77508 standard; protein; 458 AA.
DE Zebrafish TDE1 protein SEQ ID NO:3.
PN WO2003066829-A2.
PD 14-AUG-2003.
PA (DISC-) DISCOVERY GENOMICS INC.
Query Match 5.8%; Score 80.5; DB 7; Length 458;
Best Local Similarity 23.3%; Pred. No. 7.9;
RESULT 1456
ID ABU38985 standard; protein; 470 AA.
DE Protein encoded by Prokaryotic essential gene #24512.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 80.5; DB 6; Length 470;
Best Local Similarity 21.6%; Pred. No. 8.2;
RESULT 1457
ID ADS44667 standard; protein; 473 AA.
DE Bacterial polypeptide #23097.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 80.5; DB 8; Length 473;
Best Local Similarity 21.5%; Pred. No. 8.3;
RESULT 1458
ID AAU72955 standard; protein; 528 AA.
DE Neisseria meningitidis virulence protein #45.
PN WO200185772-A2.
PD 15-NOV-2001.
PA (MICR-) MICROSCIENCE LTD.
Query Match 5.8%; Score 80.5; DB 5; Length 528;
Best Local Similarity 23.3%; Pred. No. 9.6;
RESULT 1459
ID ABP79912 standard; protein; 528 AA.
DE N. gonorrhoeae amino acid sequence SEQ ID 6354.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 80.5; DB 6; Length 528;
Best Local Similarity 23.3%; Pred. No. 9.6;
RESULT 1460
ID ABR54218 standard; protein; 531 AA.
DE Human NOV21a protein SEQ ID NO:104.
PN WO2003023001-A2.
PD 20-MAR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 80.5; DB 6; Length 531;
Best Local Similarity 19.8%; Pred. No. 9.7;
RESULT 1461
ID ADN19054 standard; protein; 590 AA.
DE Bacterial polypeptide #1707.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 80.5; DB 8; Length 590;

```
Best Local Similarity 23.9%; Pred. No. 11;
RESULT 1462
ID ADN25397 standard; protein; 602 AA.
DE Bacterial polypeptide #8050.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 80.5; DB 8; Length 602;
Best Local Similarity 21.5%; Pred. No. 12;
RESULT 1463
ID ADG79602 standard; protein; 137 AA.
DE Human secreted protein of the invention SEQ ID NO:408.
PN WO200268638-A1.
PD 06-SEP-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 80; DB 5; Length 137;
Best Local Similarity 24.5%; Pred. No. 1.7;
RESULT 1464
ID ADA54634 standard; protein; 221 AA.
DE Human protein, SEQ ID 2202.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 80; DB 6; Length 221;
Best Local Similarity 24.5%; Pred. No. 3.3;
RESULT 1465
ID ABU38616 standard; protein; 266 AA.
DE Protein encoded by Prokaryotic essential gene #24143.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 80; DB 6; Length 266;
Best Local Similarity 23.8%; Pred. No. 4.3;
RESULT 1466
ID ADN46298 standard; protein; 271 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID176.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.7%; Score 80; DB 8; Length 271;
Best Local Similarity 22.2%; Pred. No. 4.4;
RESULT 1467
ID ADK48015 standard; protein; 292 AA.
DE Streptococcus pneumoniae protein, Seq ID No 4530.
PN US6699703-B1.
PD 02-MAR-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 80; DB 8; Length 292;
Best Local Similarity 18.0%; Pred. No. 4.8;
RESULT 1468
ID AAY38701 standard; protein; 307 AA.
DE Neisseria gonorrhoeae antigen encoded by partial ORF104.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.7%; Score 80; DB 2; Length 307;
Best Local Similarity 20.3%; Pred. No. 5.2;
RESULT 1469
ID ADR94835 standard; protein; 308 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 3470.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 80; DB 8; Length 308;
Best Local Similarity 18.0%; Pred. No. 5.2;
RESULT 1470
ID ABO69264 standard; protein; 325 AA.
DE Pseudomonas aeruginosa polypeptide #1439.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 80; DB 7; Length 325;
Best Local Similarity 23.8%; Pred. No. 5.6;
RESULT 1471
ID ADN17651 standard; protein; 398 AA.
DE Bacterial polypeptide #304.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 80; DB 8; Length 398;
Best Local Similarity 20.4%; Pred. No. 7.4;
RESULT 1472
ID AAY97750 standard; protein; 557 AA.
DE G. oxydans cytochrome C oxidase (COI) protein sequence.
PN EP1103603-A2.
PD 30-MAY-2001.
PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.7%; Score 80; DB 4; Length 557;
Best Local Similarity 21.2%; Pred. No. 12;
RESULT 1473
ID ADS28294 standard; protein; 902 AA.
DE Bacterial polypeptide #17327.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 80; DB 8; Length 902;
Best Local Similarity 26.6%; Pred. No. 23;
RESULT 1474
ID ADA35872 standard; protein; 241 AA.
DE Acinetobacter baumannii protein #3033.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 241;
Best Local Similarity 24.1%; Pred. No. 4.2;
RESULT 1475
ID ABU16710 standard; protein; 303 AA.
DE Protein encoded by Prokaryotic essential gene #2237.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79.5; DB 6; Length 303;
Best Local Similarity 20.7%; Pred. No. 5.8;
RESULT 1476
ID AAY37819 standard; protein; 305 AA.
DE Amino acid sequence of a Chlamydia trachomatis protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST ) GENSET.
Query Match 5.7%; Score 79.5; DB 2; Length 305;
Best Local Similarity 18.0%; Pred. No. 5.9;
RESULT 1477
ID ABU16944 standard; protein; 306 AA.
DE Protein encoded by Prokaryotic essential gene #2471.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79.5; DB 6; Length 306;
Best Local Similarity 20.4%; Pred. No. 5.9;
RESULT 1478
ID ADA35805 standard; protein; 308 AA.
DE Acinetobacter baumannii protein #2966.
PN US6562958-B1.
```

PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 308;
Best Local Similarity 20.7%; Pred. No. 5.9;
RESULT 1479
ID ADA33577 standard; protein; 315 AA.
DE Acinetobacter baumannii protein #738.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 315;
Best Local Similarity 20.4%; Pred. No. 6.1;
RESULT 1480
ID AAG71628 standard; protein; 326 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1309.
PN WO200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match 5.7%; Score 79.5; DB 4; Length 326;
Best Local Similarity 19.2%; Pred. No. 6.4;
RESULT 1481
ID ADD69607 standard; protein; 453 AA.
DE Human REMAP protein - SEQ ID 36.
PN WO2003048305-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.7%; Score 79.5; DB 7; Length 453;
Best Local Similarity 21.1%; Pred. No. 10;
RESULT 1482
ID AAU43079 standard; protein; 461 AA.
DE Propionibacterium acnes immunogenic protein #3975.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 79.5; DB 4; Length 461;
Best Local Similarity 19.4%; Pred. No. 10;
RESULT 1483
ID ABM39598 standard; protein; 461 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #4274.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.7%; Score 79.5; DB 6; Length 461;
Best Local Similarity 19.4%; Pred. No. 10;
RESULT 1484
ID ABO60912 standard; protein; 483 AA.
DE Klebsiella pneumoniae polypeptide seqid 7429.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 79.5; DB 7; Length 483;
Best Local Similarity 25.6%; Pred. No. 11;
RESULT 1485
ID ABU24876 standard; protein; 509 AA.
DE Protein encoded by Prokaryotic essential gene #10403.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79.5; DB 6; Length 509;
Best Local Similarity 23.0%; Pred. No. 12;
RESULT 1486
ID AAB96516 standard; protein; 513 AA.
DE Putative P. abyssi hydrogenase subunit #5.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 5.7%; Score 79.5; DB 4; Length 513;
Best Local Similarity 19.9%; Pred. No. 12;
RESULT 1487
ID ADO28948 standard; protein; 630 AA.
DE Mouse novel GPCR PGR25, SEQ ID NO:47.

PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 79.5; DB 8; Length 630;
Best Local Similarity 20.8%; Pred. No. 16;
RESULT 1488
ID ABB67845 standard; protein; 2210 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30327.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.7%; Score 79.5; DB 4; Length 2210;
Best Local Similarity 24.5%; Pred. No. 90;
RESULT 1489
ID ABU40578 standard; protein; 292 AA.
DE Protein encoded by Prokaryotic essential gene #26105.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79; DB 6; Length 292;
Best Local Similarity 16.5%; Pred. No. 6.3;
RESULT 1490
ID AAY90241 standard; protein; 293 AA.
DE Chlamydia antigen CPN100708.
PN WO200032794-A2.
PD 08-JUN-2000.
PA (CONN-) CONNAUGHT LAB LTD.
Query Match 5.7%; Score 79; DB 3; Length 293;
Best Local Similarity 18.3%; Pred. No. 6.3;
RESULT 1491
ID ABP62011 standard; protein; 293 AA.
DE C. pneumoniae BVH-CPN19 from strain CWL-029.
PN EP1219635-A2.
PD 03-JUL-2002.
PA (SHIR-) SHIRE BIOCHEM INC.
Query Match 5.7%; Score 79; DB 5; Length 293;
Best Local Similarity 18.3%; Pred. No. 6.3;
RESULT 1492
ID AAY38700 standard; protein; 307 AA.
DE Neisseria meningitidis strain A antigen encoded by ORF104.
PN WO9924578-A2.
PD 20-MAY-1999.
PA (CHIR-) CHIRON SPA.
Query Match 5.7%; Score 79; DB 2; Length 307;
Best Local Similarity 21.5%; Pred. No. 6.7;
RESULT 1493
ID ADH42479 standard; protein; 308 AA.
DE Novel human protein NOV69a.
PN WO2003102159-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.7%; Score 79; DB 8; Length 308;
Best Local Similarity 19.3%; Pred. No. 6.8;
RESULT 1494
ID AAG44352 standard; protein; 363 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55545.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 79; DB 3; Length 363;
Best Local Similarity 25.9%; Pred. No. 8.5;
RESULT 1495
ID AAG44351 standard; protein; 373 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55544.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 79; DB 3; Length 373;
Best Local Similarity 25.9%; Pred. No. 8.8;
RESULT 1496
ID AAG44350 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 55543.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 79; DB 3; Length 377;

Best Local Similarity 25.9%; Pred. No. 9;
RESULT 1497
ID ABU20479 standard; protein; 389 AA.
DE Protein encoded by Prokaryotic essential gene #6006.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79; DB 6; Length 389;
Best Local Similarity 20.1%; Pred. No. 9.3;
RESULT 1498
ID ADN20367 standard; protein; 390 AA.
DE Bacterial polypeptide #3020.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 79; DB 8; Length 390;
Best Local Similarity 21.5%; Pred. No. 9.4;
RESULT 1499
ID ADO29107 standard; protein; 416 AA.
DE Mouse novel GPCR HCRT1, SEQ ID NO:206.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 79; DB 8; Length 416;
Best Local Similarity 21.4%; Pred. No. 10;
RESULT 1500
ID ABU23067 standard; protein; 444 AA.
DE Protein encoded by Prokaryotic essential gene #8594.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 79; DB 6; Length 444;
Best Local Similarity 21.6%; Pred. No. 11;

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OM protein - protein search, using sw model

Run on: August 26, 2005, 17:12:21 ; Search time 41 Seconds
(without alignments)
624.236 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWWFQQLSFLPSALVIWTS.....YDTAPCPINNERTRLLSRDI 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
%			
Result No.	Score	Query Match Length DB ID	Description
1	361.5	26.0 246 2 T13747	hypothetical prote
2	288	20.7 271 2 T19654	hypothetical prote
3	120	8.6 547 2 C88456	protein W03A5.2 [i
4	103	7.4 332 2 E69312	nitrate reductase
5	98.5	7.1 1120 2 A10561	integral membrane
6	97	7.0 604 2 E72523	carbon starvation
7	96	6.9 495 2 S43882	NADH2 dehydrogenas
8	94	6.8 495 1 S16447	NADH2 dehydrogenas
9	93.5	6.7 379 2 D96506	hypothetical prote
10	93.5	6.7 429 2 F71651	putrescine-ornithi
11	93	6.7 1120 2 F90693	mechanosensitive c
12	93	6.7 1120 2 B85544	mechanosensitive c
13	93	6.7 1120 2 H64776	probable membrane
14	92.5	6.6 473 2 AE0801	probable amino aci
15	91.5	6.6 373 2 T24487	hypothetical prote
16	91.5	6.6 712 2 T02479	potassium transpor
17	90.5	6.5 614 2 E86194	hypothetical prote
18	90	6.5 400 2 C82503	hypothetical prote
19	90	6.5 492 2 S59107	NADH2 dehydrogenas
20	90	6.5 528 2 S19366	hypothetical prote
21	89.5	6.4 440 2 B64090	dicarboxylate tran
22	89.5	6.4 443 2 AE1706	hypothetical prote
23	89.5	6.4 495 2 G71019	hypothetical prote
24	89.5	6.4 599 2 T24333	hypothetical prote
25	89	6.4 428 2 A10034	probable transmemb
26	89	6.4 757 2 T42693	hypothetical prote
27	88.5	6.4 430 2 E75217	transporter PAB217
28	88.5	6.4 844 2 T23656	hypothetical prote
29	88	6.3 1165 2 A46180	adenylyl cyclase t

30	87.5	6.3	233	2	E70114	hemolysin III (ypl
31	87.5	6.3	429	2	D82181	GGDEF family prote
32	87.5	6.3	482	2	B69803	metabolite transpo
33	87.5	6.3	540	2	T24675	hypothetical prote
34	87	6.2	396	2	B91013	bicyclomycin resis
35	87	6.2	396	2	D85857	bicyclomycin resis
36	87	6.2	435	2	C95975	probable polysacch
37	87	6.2	613	2	C83496	glutathione-regula
38	86.5	6.2	400	2	C69757	transporter homolo
39	86.5	6.2	583	2	AH1151	glycerophosphoryl
40	86.5	6.2	770	2	G72589	hypothetical prote
41	86	6.2	373	2	D89865	hypothetical prote
42	86	6.2	389	2	G75133	hypothetical prote
43	86	6.2	396	1	E64987	bicyclomycin resis
44	86	6.2	703	2	E86146	F22L4.12 protein -
45	85.5	6.1	295	2	E81179	spermidine/putresc
46	85.5	6.1	296	2	AB0210	probable ABC sugar
47	85.5	6.1	498	2	S78184	NADH2 dehydrogenas
48	85	6.1	338	2	G70584	phosphate transpor
49	85	6.1	443	2	B86849	polysaccharide bios
50	85	6.1	1180	2	A47202	adenylyate cyclase
51	84.5	6.1	457	2	T46332	hypothetical prote
52	84.5	6.1	463	2	AH0189	Amino acid permeas
53	84.5	6.1	479	2	D72354	lipopolysaccharide
54	84.5	6.1	491	2	T15605	hypothetical prote
55	84.5	6.1	638	2	T11801	NADH2 dehydrogenas
56	84.5	6.1	765	2	T22800	hypothetical prote
57	84	6.0	318	2	E95218	iron-compound ABC
58	84	6.0	460	2	A71028	hypothetical prote
59	84	6.0	575	2	B83586	probable permease
60	84	6.0	597	2	H82328	hypothetical prote
61	83.5	6.0	261	2	D64166	hypothetical prote
62	83.5	6.0	295	2	A81927	probable polyamine
63	83.5	6.0	521	2	T41621	hypothetical prote
64	83.5	6.0	638	2	B34285	NADH2 dehydrogenas
65	83	6.0	305	2	AD1998	hypothetical prote
66	83	6.0	318	2	C98082	hypothetical prote
67	83	6.0	427	2	F97790	putrescine-ornithi
68	83	6.0	460	2	D75106	hypothetical prote
69	83	6.0	496	2	B83503	probable amino aci
70	83	6.0	637	2	S01509	NADH2 dehydrogenas
71	82.5	5.9	391	2	S48967	ethanolaminephosph
72	82.5	5.9	418	2	E83175	probable aromatic
73	82.5	5.9	452	2	A71877	proline/betaine tr
74	82.5	5.9	494	2	T14246	NADH2 dehydrogenas
75	82.5	5.9	596	2	S46001	probable amino aci
76	82	5.9	317	2	D84098	hypothetical prote
77	82	5.9	327	2	A82241	probable ABC trans
78	82	5.9	356	2	D86408	purine permease [i
79	82	5.9	446	2	A38244	citrate transport
80	82	5.9	461	2	H64636	proline/betaine tr
81	82	5.9	548	2	B87423	cytochrome-c oxida
82	82	5.9	557	2	T41588	probable amino-aci
83	82	5.9	573	2	T23589	hypothetical prote
84	82	5.9	693	2	T19598	hypothetical prote
85	82	5.9	1139	2	A10379	probable potassium
86	81.5	5.9	205	2	D95200	conserved hypothet
87	81.5	5.9	205	2	C98067	hypothetical prote
88	81.5	5.9	292	2	AE1539	sugar ABC transpor
89	81.5	5.9	307	2	H97018	bacitracin resista
90	81.5	5.9	351	2	C86408	F3H9.12 protein -
91	81.5	5.9	438	2	B83017	probable MFS trans
92	81.5	5.9	485	2	T24677	hypothetical prote
93	81.5	5.9	486	2	S51503	NADH2 dehydrogenas
94	81.5	5.9	734	2	T13785	NADH2 dehydrogenas
95	81	5.8	293	2	C95892	probable glycerol-
96	81	5.8	293	2	D71517	probable metal tra
97	81	5.8	438	2	H85822	probable transport
98	81	5.8	479	2	C64878	probable amino aci
99	81	5.8	479	2	T44326	hypothetical prote
100	81	5.8	487	2	E96782	hypothetical prote
101	81	5.8	544	2	T24633	hypothetical prote
102	81	5.8	710	2	T12143	NADH2 dehydrogenas

103 80.5 5.8 359 2 F90055 conserved hypothet
104 80.5 5.8 385 2 T07130 probable amino aci
105 80.5 5.8 433 2 AC0043 anaerobic C4-dicar
106 80.5 5.8 473 2 G69789 sugar transporter
107 80.5 5.8 528 2 E81186 L-lactate permease
108 80.5 5.8 590 1 QRBYP arginine transport
109 80.5 5.8 637 2 S78171 heme lyase yejR -
110 80.5 5.8 728 2 T13794 NADH2 dehydrogenas
111 80 5.7 266 2 G83178 conserved hypothet
112 80 5.7 291 2 A97387 hypothetrical prote
113 80 5.7 291 2 AB2605 hypothetrical prote
114 80 5.7 429 1 C41903 arsenical pump mem
115 80 5.7 702 2 T12141 NADH2 dehydrogenas
116 80 5.7 902 2 C83964 cation-transportin
117 80 5.7 1123 2 T48586 hypothetrical prote
118 79.5 5.7 323 2 T32279 hypothetrical prote
119 79.5 5.7 405 2 T42992 cyclin D - Caenorh
120 79.5 5.7 445 2 S77010 nickel resistance
121 79.5 5.7 499 2 F75059 NADH-dehydrogenase
122 79.5 5.7 539 1 S49495 cytochrome-c oxida
123 79.5 5.7 542 2 AG3605 potassium efflux s
124 79.5 5.7 570 2 AH2765 cytochrome-c oxida
125 79.5 5.7 598 2 E97546 cytochrome c oxida
126 79.5 5.7 741 2 T13051 NADH2 dehydrogenas
127 79.5 5.7 831 2 B40204 Na+/H+-exchanging
128 79 5.7 172 2 S55015 NADH2 dehydrogenas
129 79 5.7 183 2 A64009 hypothetrical prote
130 79 5.7 281 2 T26244 hypothetrical prote
131 79 5.7 293 2 B83783 hypothetrical prote
132 79 5.7 293 2 H72064 ABC transporter, p
133 79 5.7 293 2 C86558 metal transport pr
134 79 5.7 307 2 C81862 conserved hypothet
135 79 5.7 377 2 T49063 nodulin-like prote
136 79 5.7 390 2 H72265 hypothetrical prote
137 79 5.7 395 2 D69312 molybdopterin oxid
138 79 5.7 410 2 E84998 hypothetrical prote
139 79 5.7 438 2 B90976 shikimate transport
140 79 5.7 444 2 G82392 conserved hypothet
141 79 5.7 453 2 AF1198 conserved hypothet
142 79 5.7 473 2 T31717 hypothetrical prote
143 79 5.7 489 2 B97289 lysine-specific pe
144 79 5.7 685 2 T12139 NADH2 dehydrogenas
145 79 5.7 819 2 G69801 hypothetrical prote
146 79 5.7 2198 2 T20371 hypothetrical prote
147 78.5 5.6 169 2 H84191 hypothetrical prote
148 78.5 5.6 241 2 S00836 mcBE protein - Esc
149 78.5 5.6 366 2 C64449 cationic amino aci
150 78.5 5.6 405 2 T26678 hypothetrical prote
151 78.5 5.6 412 2 G89773 NADH dehydrogenase
152 78.5 5.6 493 2 F75113 hypothetrical prote
153 78.5 5.6 579 2 A70954 hypothetrical prote
154 78.5 5.6 622 2 E69609 cytochrome-c oxida
155 78.5 5.6 624 2 T48587 peptide transporte
156 78.5 5.6 732 2 T13814 NADH2 dehydrogenas
157 78.5 5.6 744 2 T13485 NADH2 dehydrogenas
158 78.5 5.6 1325 2 T01037 hypothetrical prote
159 78 5.6 158 2 T26519 hypothetrical prote
160 78 5.6 307 2 D81082 conserved hypothet
161 78 5.6 335 2 E81736 phospho-N-acetylmu
162 78 5.6 382 2 E97742 hypothetrical prote
163 78 5.6 388 2 G75375 hypothetrical prote
164 78 5.6 396 2 AF0785 bicyclomycin resis
165 78 5.6 414 2 S53075 probable membrane
166 78 5.6 422 2 H64489 hypothetrical prote
167 78 5.6 462 2 T48661 acetate-CoA ligase
168 78 5.6 688 2 T06299 potassium transpor
169 78 5.6 701 2 T15238 hypothetrical prote
170 77.5 5.6 212 2 E83936 hypothetrical prote
171 77.5 5.6 283 2 H95887 probable ABC trans
172 77.5 5.6 292 2 AD1182 sugar ABC transpor
173 77.5 5.6 293 2 AH0143 probable membrane
174 77.5 5.6 296 2 C95326 AttA2-like ABC tra
175 77.5 5.6 335 2 A72289 oligopeptide ABC t

176 77.5 5.6 363 2 A72771 hypothetrical prote
177 77.5 5.6 461 2 H85755 probable amino aci
178 77.5 5.6 464 2 C83605 probable transport
179 77.5 5.6 479 2 A90863 probable amino aci
180 77.5 5.6 499 2 AG0882 probable amino aci
181 77.5 5.6 506 2 F64862 hypothetrical prote
182 77.5 5.6 510 2 D96741 hypothetrical prote
183 77.5 5.6 510 2 E71695 sodium/solute symp
184 77.5 5.6 513 2 A82432 probable hexose tr
185 77.5 5.6 526 2 T01853 cytochrome-c oxida
186 77.5 5.6 532 1 S49345 cytochrome-c oxida
187 77.5 5.6 535 2 S76103 hypothetrical prote
188 77.5 5.6 649 2 A69478 NADH2 dehydrogenas
189 77.5 5.6 717 2 T46172 phenylalanine ammo
190 77.5 5.6 1118 2 B83018 conserved hypothet
191 77 282 2 AD1231 B. subtilis YxkD p
192 77 332 2 D95973 probable sugar upt
193 77 417 2 F90270 amino acid permeas
194 77 438 2 B69855 amino acid permeas
195 77 438 2 G64962 shikimate transpor
196 77 471 2 H90502 phosphate transpor
197 77 519 2 JQ0124 membrane protein S
198 77 551 1 A55582 cytochrome-c oxida
199 77 579 2 AB2177 hypothetrical prote
200 77 662 2 H84984 bo-type ubiquinol
201 77 710 2 T20635 hypothetrical prote
202 77 739 2 T13038 NADH2 dehydrogenas
203 77 749 2 E71275 hypothetrical integ
204 77 915 2 H96709 hypothetrical prote
205 77 936 2 T26521 hypothetrical prote
206 76.5 152 2 C72681 hypothetrical prote
207 76.5 269 2 H69768 conserved hypothet
208 76.5 284 2 G64052 probable formate t
209 76.5 289 2 T02095 transmembrane prot
210 76.5 300 2 S40858 hypothetrical 32.9K
211 76.5 300 2 H91233 probable transport
212 76.5 300 2 H86080 probable transport
213 76.5 301 2 B82235 conserved hypothet
214 76.5 301 2 T27585 hypothetrical prote
215 76.5 305 2 D83699 hypothetrical prote
216 76.5 334 2 A75142 oligopeptide trans
217 76.5 370 2 AB3334 daunorubicin resis
218 76.5 377 2 C89456 protein F55A4.8 [i
219 76.5 382 2 B82177 Na+/H+ antiporter
220 76.5 395 2 AD0678 probable membrane
221 76.5 431 2 H84069 hypothetrical prote
222 76.5 474 2 F64119 NAD(P) transhydrog
223 76.5 475 2 E69643 histidine permease
224 76.5 495 2 AD0402 glycerol kinase (E
225 76.5 548 2 B72542 probable cytochrom
226 76.5 725 2 S64124 probable membrane
227 76.5 746 2 T13698 NADH2 dehydrogenas
228 76.5 855 2 T47534 hypothetrical prote
229 76.5 1187 2 T20544 hypothetrical prote
230 76.5 1342 2 E85614 cell division prot
231 76.5 1342 2 G90750 cell division prot
232 76 261 2 A64066 probable membrane
233 76 275 2 C97028 probable metal-bin
234 76 281 2 AB1585 B. subtilis YxkD p
235 76 282 2 D97767 hypothetrical prote
236 76 336 2 T23902 hypothetrical prote
237 76 365 2 F82210 cell division prot
238 76 415 2 G83568 probable permease
239 76 447 2 C84306 hypothetrical prote
240 76 452 2 S46037 prephenate dehydro
241 76 480 2 G83414 cytochrome-c oxida
242 76 502 2 JN0113 nicotinic acetylch
243 76 558 2 S08270 cytochrome-c oxida
244 76 578 2 T13664 NADH2 dehydrogenas
245 76 617 2 T20409 hypothetrical prote
246 76 659 2 E85889 probable oxidoredu
247 76 659 2 B91045 NADH2 dehydrogenas
248 76 669 1 DNMUUS

249 76 5.5 956 2 A89153 protein C24B5.3 [i
250 76 5.5 958 2 AC0204 probable integral
251 76 5.5 966 2 H97717 hypothetical prote
252 76 5.5 971 2 H71719 hypothetical prote
253 76 5.5 1052 2 T50127 hypothetical prote
254 76 5.5 1074 2 T45094 probable arabinosy
255 76 5.5 1166 2 A49201 adenylate cyclase
256 75.5 5.4 210 2 T01623 hypothetical prote
257 75.5 5.4 237 2 A99737 hypothetical prote
258 75.5 5.4 237 2 B85587 hypothetical prote
259 75.5 5.4 240 2 D71939 hypothetical prote
260 75.5 5.4 252 2 B47188 MHC class II histo
261 75.5 5.4 295 1 QQSABT hypothetical prote
262 75.5 5.4 296 2 E83049 conserved hypothet
263 75.5 5.4 297 2 AE0400 probable membrane
264 75.5 5.4 322 2 A97657 ferrichrome ABC tr
265 75.5 5.4 322 2 AI2880 ABC transporter, m
266 75.5 5.4 338 2 C83785 ferrichrome ABC tr
267 75.5 5.4 397 2 D69538 arsenite transport
268 75.5 5.4 432 2 A42476 hypothetical prote
269 75.5 5.4 432 2 AD0766 probable O-antigen
270 75.5 5.4 441 2 B71027 probable nfeD prot
271 75.5 5.4 454 2 E85826 probable amino aci
272 75.5 5.4 454 2 H90980 probable amino aci
273 75.5 5.4 454 2 E64966 probable amino aci
274 75.5 5.4 454 2 AG0763 probable amino aci
275 75.5 5.4 459 2 S42238 tetracyclin resist
276 75.5 5.4 476 2 S23576 melibiose transpor
277 75.5 5.4 492 2 AC0768 probable transmemb
278 75.5 5.4 513 2 I39534 hypothetical prote
279 75.5 5.4 532 2 D95287 conserved hypothet
280 75.5 5.4 567 2 B81408 probable thiol-dis
281 75.5 5.4 676 1 S54750 cytochrome c-type
282 75.5 5.4 735 2 F84726 probable Na+/H+ an
283 75.5 5.4 740 2 T12223 NADH2 dehydrogenas
284 75.5 5.4 832 2 A40205 Na+/H+-exchanging
285 75.5 5.4 914 2 I40529 penicillin-binding
286 75.5 5.4 932 2 T25941 hypothetical prote
287 75 5.4 262 2 B83827 hypothetical prote
288 75 5.4 289 2 T12037 probable aquaporin
289 75 5.4 291 2 T04139 transmembrane prot
290 75 5.4 298 2 S75972 hypothetical prote
291 75 5.4 322 2 B98193 sugar ABC transpor
292 75 5.4 322 2 AH3093 hypothetical prote
293 75 5.4 395 2 S73531 CDP-diglyceride sy
294 75 5.4 398 2 B71193 hypothetical prote
295 75 5.4 429 1 B41902 arsenical pump mem
296 75 5.4 432 2 H71092 hypothetical prote
297 75 5.4 451 2 E90171 inorganic phosphat
298 75 5.4 461 2 AF1179 hexose phosphate t
299 75 5.4 494 2 A82294 probable carbon st
300 75 5.4 507 2 AI1739 amino acid antipor
301 75 5.4 559 2 T33168 hypothetical prote
302 75 5.4 599 2 T48383 uracil transporter
303 75 5.4 625 2 D45335 cytochrome-c oxida
304 75 5.4 643 2 E69373 conserved hypothet
305 75 5.4 917 2 I49699 glycoprotein 130 -
306 75 5.4 1056 2 G84865 hypothetical prote
307 75 5.4 1294 2 S77690 probable membrane
308 74.5 5.4 174 2 F90494 conserved hypothet
309 74.5 5.4 288 2 T09794 major intrinsic pr
310 74.5 5.4 293 2 A96209 motC protein [limp
311 74.5 5.4 293 2 AH3077 hypothetical prote
312 74.5 5.4 305 2 B33465 lic-1 protein B -
313 74.5 5.4 311 2 F70184 ribose/galactose A
314 74.5 5.4 323 2 T31697 phospho-N-acetylmu
315 74.5 5.4 324 1 C47691 lipopolysaccharide
316 74.5 5.4 325 2 F82558 CT838 hypothetical
317 74.5 5.4 366 2 H86614 conserved hypothet
318 74.5 5.4 366 2 C72009 conserved hypothet
319 74.5 5.4 367 2 T13813 NADH2 dehydrogenas
320 74.5 5.4 399 2 T27853 hypothetical prote
321 74.5 5.4 409 1 F69814 fosmidmycin resist

322 74.5 5.4 411 2 T03836 phosphate/phosphoe
323 74.5 5.4 439 2 AB0389 branched-chain ami
324 74.5 5.4 447 2 T19112 hypothetical prote
325 74.5 5.4 469 1 BDEC melibiose carrier
326 74.5 5.4 469 2 C86107 melibiose permease
327 74.5 5.4 469 2 F91266 melibiose permease
328 74.5 5.4 476 2 AG0502 probable amino-aci
329 74.5 5.4 544 2 T32895 hypothetical prote
330 74.5 5.4 560 2 T32727 hypothetical prote
331 74.5 5.4 726 2 T12215 NADH2 dehydrogenas
332 74.5 5.4 889 2 AD2215 two-component hybr
333 74.5 5.4 953 2 S19427 probable membrane
334 74 5.3 277 2 E72030 conserved hypothet
335 74 5.3 277 2 A86594 CT560 hypothetical
336 74 5.3 281 2 H90387 hypothetical prote
337 74 5.3 296 2 C69635 transcription repr
338 74 5.3 303 2 T25501 hypothetical prote
339 74 5.3 322 1 A29928 membrane-associate
340 74 5.3 370 2 H84351 hypothetical prote
341 74 5.3 380 2 S34964 rfc protein - Shig
342 74 5.3 400 2 F86887 hypothetical prote
343 74 5.3 401 2 E82951 probable MFS trans
344 74 5.3 404 2 A36865 ammonium transport
345 74 5.3 407 2 G81010 conserved hypothet
346 74 5.3 425 2 H71554 hypothetical prote
347 74 5.3 431 2 T41614 malate permease -
348 74 5.3 437 2 G82032 probable permease
349 74 5.3 446 2 A42661 citrate carrier pr
350 74 5.3 446 2 AD0509 citrate-sodium sym
351 74 5.3 446 2 B42661 citrate carrier pr
352 74 5.3 459 2 T11084 NADH2 dehydrogenas
353 74 5.3 473 2 AG0948 probable membrane
354 74 5.3 508 2 A83839 hypothetical prote
355 74 5.3 530 2 F85768 PTS system, maltos
356 74 5.3 530 2 A99920 PTS system, maltos
357 74 5.3 532 2 H96840 hypothetical prote
358 74 5.3 542 2 F90457 hypothetical prote
359 74 5.3 592 2 T25837 hypothetical prote
360 74 5.3 612 2 C90419 glucan 1,4 alpha g
361 74 5.3 740 2 AH0600 probable membrane
362 74 5.3 817 2 T51787 hypothetical prote
363 74 5.3 908 2 S51293 probable membrane
364 74 5.3 947 2 H85088 hypothetical prote
365 73.5 5.3 218 1 D69372 osmoprotection pro
366 73.5 5.3 240 2 A64652 hypothetical prote
367 73.5 5.3 299 2 B83323 hypothetical prote
368 73.5 5.3 329 2 AD0442 probable branched-
369 73.5 5.3 337 2 T23942 hypothetical prote
370 73.5 5.3 343 2 G86709 hypothetical prote
371 73.5 5.3 363 2 AF2457 hypothetical prote
372 73.5 5.3 372 2 A98157 probable permease
373 73.5 5.3 372 2 AH3130 ABC transporter, m
374 73.5 5.3 391 2 S30046 potassium channel
375 73.5 5.3 409 2 T03718 suppressor 2 prote
376 73.5 5.3 423 2 C81266 probable efflux pr
377 73.5 5.3 425 2 C65100 hypothetical 46.6
378 73.5 5.3 426 2 D72049 phosphate permease
379 73.5 5.3 443 2 F85972 probable transport
380 73.5 5.3 443 2 G91127 probable transport
381 73.5 5.3 463 2 F90285 metabolite transpo
382 73.5 5.3 476 2 AC1023 melibiose carrier
383 73.5 5.3 477 2 F82200 cytochrome-c oxida
384 73.5 5.3 498 2 F89861 Na+/H+-antipoter
385 73.5 5.3 507 2 B97765 aDP,ATP carrier pr
386 73.5 5.3 522 2 D86263 F13K23.21 protein
387 73.5 5.3 526 2 S74025 conserved hypothet
388 73.5 5.3 526 2 T29433 hypothetical prote
389 73.5 5.3 547 2 AB2639 pH adaption potass
390 73.5 5.3 548 2 C97421 phaD protein (X933
391 73.5 5.3 592 2 E75032 carbon starvation
392 73.5 5.3 607 2 S19585 serotonin transpor
393 73.5 5.3 607 2 S63395 probable membrane
394 73.5 5.3 630 2 S30604 neurotransmitter t

395 73.5 5.3 674 2 E82954 conserved hypothet
396 73.5 5.3 699 2 T13730 NADH2 dehydrogenas
397 73.5 5.3 875 2 H90371 proteinase [import
398 73.5 5.3 885 2 B69783 transporter homolo
399 73.5 5.3 889 2 T20123 hypothetical prote
400 73.5 5.3 1099 2 A55405 adenylate cyclase
401 73.5 5.3 1128 2 T04922 hypothetical prote
402 73.5 5.3 1343 2 AF0611 cell division prot
403 73.5 5.3 2818 2 B55282 neurofibromatosis-
404 73.5 5.3 2820 2 JC5196 neurofibromin I -
405 73.5 5.3 2825 2 I54352 neurofibromin - mo
406 73 5.2 140 2 C83199 hypothetical prote
407 73 5.2 193 2 B91170 hypothetical membr
408 73 5.2 193 2 B86016 hypothetical prote
409 73 5.2 261 2 AC0251 high-affinity zinc
410 73 5.2 262 2 F97151 ABC transported MD
411 73 5.2 282 2 H71696 hypothetical prote
412 73 5.2 283 2 D83009 probable permease
413 73 5.2 292 2 C95147 licB protein [mpo
414 73 5.2 294 2 D81434 probable 4-hydroxy
415 73 5.2 296 2 A98015 hypothetical prote
416 73 5.2 301 2 AH2064 hypothetical prote
417 73 5.2 311 2 T33436 hypothetical prote
418 73 5.2 364 2 D95959 conserved hypothet
419 73 5.2 384 2 S37608 NADH2 dehydrogenas
420 73 5.2 399 2 AE0396 probable sugar tra
421 73 5.2 401 2 T49929 hypothetical prote
422 73 5.2 436 2 S77639 exopolysaccharide
423 73 5.2 437 2 D86633 amino acid permeas
424 73 5.2 453 2 AD1556 conserved hypothet
425 73 5.2 456 2 H97735 hypothetical prote
426 73 5.2 470 2 B86118 transport of D-ala
427 73 5.2 470 2 B91277 D-serine/D-alanine
428 73 5.2 470 2 S56433 D-serine/D-alanine
429 73 5.2 495 1 S25942 NADH2 dehydrogenas
430 73 5.2 507 2 AB1370 amino acid antipor
431 73 5.2 574 2 T05964 probable low-affin
432 73 5.2 633 2 T19189 hypothetical prote
433 73 5.2 639 2 G88839 protein C10C6.5 [i
434 73 5.2 700 2 T13668 NADH2 dehydrogenas
435 73 5.2 732 2 T14233 NADH2 dehydrogenas
436 73 5.2 1564 2 T27121 hypothetical prote
437 73 5.2 3079 1 R6BY12 probable GTPase-ac
438 73 5.2 3898 1 GNWVHB genome polypept
439 72.5 5.2 118 2 G64394 hypothetical prote
440 72.5 5.2 235 2 F95230 membrane protein [i
441 72.5 5.2 235 2 A99095 conserved hypothet
442 72.5 5.2 235 2 AF0598 probable membrane
443 72.5 5.2 271 2 T11704 NADH2 dehydrogenas
444 72.5 5.2 284 2 AH0680 probable dimethyl
445 72.5 5.2 286 2 B99213 cytochrome C oxida
446 72.5 5.2 297 2 F82039 ribonuclease BN VC
447 72.5 5.2 308 2 AF0461 probable membrane
448 72.5 5.2 330 2 D95902 probable sugar ABC
449 72.5 5.2 347 2 AD2201 hypothetical prote
450 72.5 5.2 368 2 T13815 NADH2 dehydrogenas
451 72.5 5.2 375 2 B40205 Na+/H+-exchangin
452 72.5 5.2 421 2 T22969 hypothetical prote
453 72.5 5.2 434 2 D65132 hypothetical 46.5
454 72.5 5.2 458 2 B90623 NADH dehydrogenase
455 72.5 5.2 459 2 T19110 hypothetical prote
456 72.5 5.2 461 2 G85059 probable sugar tra
457 72.5 5.2 461 2 S75711 hypothetical prote
458 72.5 5.2 491 2 H83979 lysine decarboxyla
459 72.5 5.2 494 1 F69355 Na+/H+ antipor
460 72.5 5.2 498 2 B89832 hypothetical prote
461 72.5 5.2 523 2 A11970 ABC-type transport
462 72.5 5.2 615 2 S77084 ABC transporter (p
463 72.5 5.2 646 2 B70001 ABC transporter (p
464 72.5 5.2 682 2 T12715 NADH2 dehydrogenas
465 72.5 5.2 684 2 T13491 NADH2 dehydrogenas
466 72.5 5.2 704 2 T13665 NADH2 dehydrogenas
467 72.5 5.2 736 2 T12716 NADH2 dehydrogenas

468 72.5 5.2 741 2 T13085 NADH2 dehydrogenas
469 72.5 5.2 743 2 T13073 NADH2 dehydrogenas
470 72.5 5.2 744 2 T13040 NADH2 dehydrogenas
471 72.5 5.2 744 2 T13757 NADH2 dehydrogenas
472 72.5 5.2 917 2 T17244 hypothetical prote
473 72.5 5.2 923 2 C97487 hypothetical prote
474 72.5 5.2 923 2 AC2705 conserved hypothet
475 72.5 5.2 953 2 S54478 probable membrane
476 72.5 5.2 958 2 A70634 probable mmpL1 pro
477 72.5 5.2 978 2 JC8067 mitochondrial Cl-t
478 72.5 5.2 1148 2 H90175 NADH dehydrogenase
479 72.5 5.2 1329 2 A64828 cell division prot
480 72.5 5.2 2658 2 A86216 hypothetical prote
481 72 5.2 215 2 F75166 membrane protein -
482 72 5.2 242 2 S49598 hypothetical prote
483 72 5.2 249 2 A71234 hypothetical prote
484 72 5.2 252 2 A71165 probable dimethyl
485 72 5.2 257 2 AC1024 FP0 protein - fowl
486 72 5.2 260 1 WMVZP0 probable membrane
487 72 5.2 261 2 S62047 hypothetical prote
488 72 5.2 282 2 D98058 hypothetical prote
489 72 5.2 286 2 T23066 ferrichrome ABC tr
490 72 5.2 315 2 B83778 conserved hypothet
491 72 5.2 339 2 E86761 hypothetical prote
492 72 5.2 339 2 T23244 G protein-coupled
493 72 5.2 355 2 A55733 hypothetical prote
494 72 5.2 359 2 AF3044 ribose ABC transpo
495 72 5.2 361 2 C84246 ferrichrome ABC tr
496 72 5.2 367 2 C82943 mtlK protein (AF00
497 72 5.2 374 2 F98241 hypothetical prote
498 72 5.2 378 2 T34372 probable transport
499 72 5.2 417 2 F90916 membrane protein y
500 72 5.2 417 2 F64915 probable transport
501 72 5.2 421 2 C85765 ammonium transport
502 72 5.2 421 2 B84129 sugar transporter
503 72 5.2 431 2 C82432 modulation protein
504 72 5.2 440 2 C75107 conserved hypothet
505 72 5.2 440 2 C82410 hypothetical prote
506 72 5.2 444 2 T24076 probable gluconate
507 72 5.2 447 2 AE0094 cytochrome D ubiqu
508 72 5.2 453 2 H71732 sodium-glutamate s
509 72 5.2 463 2 H69822 NADH2 dehydrogenas
510 72 5.2 482 2 T17022 adp, ATP carrier p
511 72 5.2 507 2 B71695 hypothetical prote
512 72 5.2 524 2 AD1897 phosphotransferase
513 72 5.2 530 1 G64918 high affinity nitr
514 72 5.2 530 2 T51836 probable 3'-5' exo
515 72 5.2 582 2 H96604 hypothetical prote
516 72 5.2 602 2 AC2313 hypothetical prote
517 72 5.2 608 2 S76192 NADH2 dehydrogenas
518 72 5.2 614 2 T13727 cytochrome-c oxida
519 72 5.2 620 2 F83976 hypothetical prote
520 72 5.2 628 2 AG2707 mitochondrial tran
521 72 5.2 629 2 H97489 hypothetical prote
522 72 5.2 641 2 AG2164 transporter, trunc
523 72 5.2 644 2 B97885 NADH2 dehydrogenas
524 72 5.2 681 2 T13566 NADH2 dehydrogenas
525 72 5.2 689 2 T11917 hypothetical prote
526 72 5.2 692 2 T33786 NADH2 dehydrogenas
527 72 5.2 696 2 T12160 NADH2 dehydrogenas
528 72 5.2 698 2 T12565 NADH2 dehydrogenas
529 72 5.2 698 2 T12161 NADH2 dehydrogenas
530 72 5.2 700 2 T13763 NADH2 dehydrogenas
531 72 5.2 719 2 T13793 NADH2 dehydrogenas
532 72 5.2 796 2 S62464 conserved hypothet
533 72 5.2 906 2 S35312 coatomer complex b
534 72 5.2 2150 2 T08165 RNA1 polypept
535 71.5 5.1 213 2 A71049 hypothetical prote
536 71.5 5.1 232 2 E86825 hypothetical prote
537 71.5 5.1 260 2 H89899 phosphatidate cyti
538 71.5 5.1 281 2 A55862 aarA protein - Pro
539 71.5 5.1 283 2 B69769 hypothetical prote
540 71.5 5.1 285 2 A11127 Staphylococcus xyl

687	70.5	5.1	674	2	AC1913	two-component sens	760	70	5.0	2201	1	GNYYA9	genome polyprotein
688	70.5	5.1	683	2	T12158	NADH2 dehydrogenas	761	69.5	5.0	202	2	F86347	hypothetical prote
689	70.5	5.1	704	2	T13581	NADH2 dehydrogenas	762	69.5	5.0	210	2	H81406	probable integral
690	70.5	5.1	718	2	S48726	phenylalanine ammo	763	69.5	5.0	215	2	S75345	hypothetical prote
691	70.5	5.1	733	2	T12213	NADH2 dehydrogenas	764	69.5	5.0	222	2	E72228	hypothetical prote
692	70.5	5.1	737	2	T13504	NADH2 dehydrogenas	765	69.5	5.0	224	2	B71191	hypothetical prote
693	70.5	5.1	738	2	C95936	conserved hypothet	766	69.5	5.0	256	2	S26742	tonoplast intrinsi
694	70.5	5.1	740	1	DENTN5	NADH2 dehydrogenas	767	69.5	5.0	260	2	G64690	type IIS restricti
695	70.5	5.1	741	2	T12610	NADH2 dehydrogenas	768	69.5	5.0	265	2	AF2007	hypothetical prote
696	70.5	5.1	741	2	T12702	NADH2 dehydrogenas	769	69.5	5.0	268	2	A70417	hypothetical prote
697	70.5	5.1	741	2	T13233	NADH2 dehydrogenas	770	69.5	5.0	285	1	C32804	prephenate dehydra
698	70.5	5.1	741	2	T13569	NADH2 dehydrogenas	771	69.5	5.0	285	2	AE1488	Staphylococcus xyl
699	70.5	5.1	921	2	T19694	hypothetical prote	772	69.5	5.0	286	2	F87075	membrane transport
700	70.5	5.1	1134	2	A41350	adenylate cyclase	773	69.5	5.0	287	2	T09791	drought-induced ma
701	70.5	5.1	1681	2	A55138	sodium channel mNa	774	69.5	5.0	292	2	G75288	hypothetical prote
702	70.5	5.1	1781	1	A34374	DNA-directed RNA p	775	69.5	5.0	294	2	S76277	ycf38 protein - Sy
703	70.5	5.1	2143	2	G96595	hypothetical prote	776	69.5	5.0	308	2	S16648	dipeptide transport
704	70	5.0	98	2	T17099	NADH2 dehydrogenas	777	69.5	5.0	315	2	F72374	conserved hypothet
705	70	5.0	160	2	F72322	hypothetical prote	778	69.5	5.0	317	2	S72851	hypothetical prote
706	70	5.0	169	2	AB2739	acetyltransferase	779	69.5	5.0	325	2	T14227	NADH2 dehydrogenas
707	70	5.0	209	2	H97519	hypothetical prote	780	69.5	5.0	329	2	T11350	NADH2 dehydrogenas
708	70	5.0	240	1	QQBEG3	HWLF4 protein - hu	781	69.5	5.0	334	2	T19955	hypothetical prote
709	70	5.0	245	2	A90527	hypothetical prote	782	69.5	5.0	340	2	AE0353	probable membrane
710	70	5.0	250	2	C91020	hypothetical prote	783	69.5	5.0	351	2	T11794	NADH2 dehydrogenas
711	70	5.0	251	2	AH0575	2,3-dihydro-2,3-di	784	69.5	5.0	353	2	S65297	probable membrane
712	70	5.0	254	2	B70235	hypothetical prote	785	69.5	5.0	358	2	T29744	hypothetical prote
713	70	5.0	273	2	A72378	conserved hypothet	786	69.5	5.0	371	2	H97452	cytochrome c oxida
714	70	5.0	282	2	A99205	hypothetical prote	787	69.5	5.0	372	2	G82790	hypothetical prote
715	70	5.0	287	2	T12440	mipC protein - com	788	69.5	5.0	385	2	AE2717	permease [imported
716	70	5.0	320	2	T20176	hypothetical prote	789	69.5	5.0	385	2	H97498	permease AGR_C 211
717	70	5.0	325	2	C98135	hypothetical prote	790	69.5	5.0	393	1	A48357	nonstructural prot
718	70	5.0	325	2	AH3152	hypothetical prote	791	69.5	5.0	398	2	C90349	multidrug-efflux t
719	70	5.0	344	2	AE3228	agrocinopine synth	792	69.5	5.0	415	2	A39412	tryptophan transpo
720	70	5.0	344	2	S51948	hypothetical prote	793	69.5	5.0	420	2	AI2458	hypothetical prote
721	70	5.0	345	2	H95381	probable iron upta	794	69.5	5.0	426	2	E86575	phosphate permease
722	70	5.0	397	2	AF2016	hypothetical prote	795	69.5	5.0	439	2	A64769	branched-chain ami
723	70	5.0	413	2	H81659	branched-chain ami	796	69.5	5.0	439	2	C90685	branched-chain ami
724	70	5.0	427	2	S74444	hypothetical prote	797	69.5	5.0	439	2	G85535	branched-chain ami
725	70	5.0	442	2	E85864	probable transport	798	69.5	5.0	440	2	H90253	NADH-Ubiquinone/pl
726	70	5.0	443	2	H85485	probable transport	799	69.5	5.0	443	2	AG1335	hypothetical prote
727	70	5.0	443	2	H90634	probable transport	800	69.5	5.0	448	2	A69747	ABC transporter (p
728	70	5.0	456	2	F97810	magnesium transpor	801	69.5	5.0	458	2	B81409	probable transmemb
729	70	5.0	458	2	A37869	alpha-2B-adrenergi	802	69.5	5.0	459	2	S10196	NADH2 dehydrogenas
730	70	5.0	459	2	T11110	NADH2 dehydrogenas	803	69.5	5.0	470	2	C87683	conserved hypothet
731	70	5.0	459	2	S28025	light harvesting c	804	69.5	5.0	472	2	B91091	L-arabinose isomer
732	70	5.0	467	2	F91228	probable permease	805	69.5	5.0	472	2	E85936	L-arabinose isomer
733	70	5.0	503	2	AB2734	NADH dehydrogenase	806	69.5	5.0	472	2	B26430	L-arabinose isomer
734	70	5.0	503	2	D97515	NADH dehydrogenase	807	69.5	5.0	475	2	E83450	cytochrome-c oxida
735	70	5.0	519	2	F84222	quinone oxidoreduc	808	69.5	5.0	478	2	AC3395	NADH2 dehydrogenas
736	70	5.0	522	2	B83987	ABC transporter (p	809	69.5	5.0	482	2	T45295	cytochrome-c oxida
737	70	5.0	539	2	E97025	spoVB related memb	810	69.5	5.0	493	2	S52421	amino acid transpo
738	70	5.0	539	2	S67049	probable membrane	811	69.5	5.0	507	2	T48645	glycine betaine tr
739	70	5.0	576	2	B71420	hypothetical prote	812	69.5	5.0	507	2	AD1336	glycine betaine tr
740	70	5.0	600	2	T32343	hypothetical prote	813	69.5	5.0	515	2	T03717	GTP-binding protei
741	70	5.0	614	2	B84949	NADH2 dehydrogenas	814	69.5	5.0	536	2	A71491	probable integral
742	70	5.0	658	2	B86599	metal transport p-	815	69.5	5.0	570	2	S42708	proline transport
743	70	5.0	658	2	D72026	metal transport p-	816	69.5	5.0	570	2	S04547	proline transport
744	70	5.0	670	2	JQ1447	NADH2 dehydrogenas	817	69.5	5.0	572	2	AB2671	cytochrome-c oxida
745	70	5.0	683	2	C81515	cation-transportin	818	69.5	5.0	591	2	S14115	NADH2 dehydrogenas
746	70	5.0	688	2	T12670	NADH2 dehydrogenas	819	69.5	5.0	591	2	S43506	hypothetical prote
747	70	5.0	698	2	T12556	NADH2 dehydrogenas	820	69.5	5.0	591	2	S77332	NADH2 dehydrogenas
748	70	5.0	700	2	T13702	NADH2 dehydrogenas	821	69.5	5.0	615	2	T11125	NADH2 dehydrogenas
749	70	5.0	705	2	T13494	NADH2 dehydrogenas	822	69.5	5.0	627	2	S67257	proline transport
750	70	5.0	732	2	T12194	NADH2 dehydrogenas	823	69.5	5.0	631	2	S75742	hypothetical prote
751	70	5.0	738	2	T14230	NADH2 dehydrogenas	824	69.5	5.0	643	2	S70592	NADH2 dehydrogenas
752	70	5.0	744	2	A81719	exodeoxyribonuclea	825	69.5	5.0	654	2	T14202	NADH2 dehydrogenas
753	70	5.0	782	2	T25925	hypothetical prote	826	69.5	5.0	686	2	T13680	NADH2 dehydrogenas
754	70	5.0	836	2	E89453	protein F35H12.3 l	827	69.5	5.0	701	2	T12296	NADH2 dehydrogenas
755	70	5.0	860	2	AB2044	adenylate cyclase	828	69.5	5.0	718	2	A99195	NADH2 dehydrogenas
756	70	5.0	1018	2	T19693	hypothetical prote	829	69.5	5.0	736	2	T12214	hypothetical prote
757	70	5.0	1070	2	B86922	probable arabinosy	830	69.5	5.0	741	2	T12706	NADH2 dehydrogenas
758	70	5.0	1155	2	B71720	hypothetical prote	831	69.5	5.0	741	2	T13086	NADH2 dehydrogenas
759	70	5.0	2108	2	S72458	sodium channel pro	832	69.5	5.0	741	2		

833 69.5 5.0 741 2 T13372 NADH2 dehydrogenas
834 69.5 5.0 744 2 T13682 NADH2 dehydrogenas
835 69.5 5.0 747 2 E91049 probable cytochrom
836 69.5 5.0 747 2 A85894 probable cytochrom
837 69.5 5.0 809 1 SYBYQT glutamine-tRNA lig
838 69.5 5.0 970 2 AI3605 potassium efflux s
839 69.5 5.0 1302 2 B41249 multidrug resistanc
840 69.5 5.0 1645 2 T31339 carbamoyl-phosphat
841 69.5 5.0 1827 2 A35694 cut1 protein - fis
842 69.5 5.0 1828 2 T41455 cut1 protein - fis
843 69 5.0 139 2 T31033 hypothetical prote
844 69 5.0 171 2 AF2434 hypothetical prote
845 69 5.0 233 2 S77443 cytochrome-c oxida
846 69 5.0 233 2 AH1068 probable membrane
847 69 5.0 236 2 S42069 TEGT protein - rat
848 69 5.0 254 2 C84315 hypothetical prote
849 69 5.0 260 2 AG0434 probable membrane
850 69 5.0 281 2 D64426 phosphate transpor
851 69 5.0 288 2 H72092 prolipoprotein dia
852 69 5.0 288 2 G86529 prolipoprotein dia
853 69 5.0 290 2 T09260 aquaporin-like tra
854 69 5.0 292 2 D81575 prolipoprotein dia
855 69 5.0 296 1 BVECPT phosphate transpor
856 69 5.0 296 2 F91211 hypothetical prote
857 69 5.0 296 2 F86057 hypothetical prote
858 69 5.0 299 2 T06960 probable membrane
859 5.0 305 2 F70030 conserved hypothet
860 69 5.0 308 2 C86561 phosphatidate cyti
861 69 5.0 308 2 H72062 phosphatidate cyti
862 69 5.0 313 2 H71341 conserved hypothet
863 69 5.0 347 2 T29415 hypothetical prote
864 69 5.0 364 2 D96973 spore germination
865 69 5.0 369 2 F69478 NADH2 dehydrogenas
866 69 5.0 387 2 E83679 multidrug-efflux t
867 69 5.0 389 2 T51355 membrane protein l
868 69 5.0 391 2 AB1285 transmembrane tran
869 69 5.0 396 2 F83130 probable MFS trans
870 69 5.0 397 2 E81223 conserved hypothet
871 69 5.0 397 2 B81994 probable transmemb
872 69 5.0 411 2 F97088 sugar-proton sympo
873 69 5.0 416 2 C81324 ubiquinol-cytochro
874 69 5.0 429 2 AI0792 probable transport
875 69 5.0 431 2 A84380 hypothetical prote
876 69 5.0 432 2 C85087 hypothetical prote
877 69 5.0 443 2 E64725 yaaU protein - Esc
878 69 5.0 449 2 AE1707 PTS system galacti
879 69 5.0 451 2 E81781 probable integral
880 69 5.0 451 2 A81206 sugar transporter,
881 69 5.0 455 2 B90619 NADH dehydrogenase
882 69 5.0 458 2 B96643 hypothetical prote
883 69 5.0 462 2 D86814 transport protein
884 69 5.0 464 2 C40630 GDP-mannose pyroph
885 69 5.0 473 2 T03611 cyclin, B-type - c
886 69 5.0 478 2 T29174 hypothetical prote
887 69 5.0 482 2 C90067 hypothetical prote
888 69 5.0 483 2 A81352 integral membrane
889 69 5.0 487 2 S40820 probable permease
890 69 5.0 488 1 H64537 cytochrome-c oxida
891 69 5.0 488 2 G71969 cytochrome-c oxida
892 69 5.0 492 2 AD3055 succinoglycan bios
893 69 5.0 495 2 S75340 NADH2 dehydrogenas
894 69 5.0 498 2 H82494 probable NADH dehy
895 69 5.0 509 2 D86978 hypothetical prote
896 69 5.0 516 2 G82182 probable NADH dehy
897 69 5.0 522 2 A98231 succinoglycan bios
898 69 5.0 528 2 T34941 probable Na+/H+ an
899 69 5.0 554 2 S03809 cytochrome-c oxida
900 69 5.0 588 2 A43740 DG42 protein - Afr
901 69 5.0 591 2 G97748 virD4 protein [imp
902 69 5.0 605 2 H95240 conserved hypothet
903 69 5.0 605 2 A99705 hypothetical prote
904 69 5.0 642 2 T33262 hypothetical prote
905 69 5.0 652 2 C97087 probable permease

906 69 5.0 670 1 DNOBU5 NADH2 dehydrogenas
907 69 5.0 677 2 T11231 NADH2 dehydrogenas
908 69 5.0 684 2 T13695 NADH2 dehydrogenas
909 69 5.0 691 2 T12293 NADH2 dehydrogenas
910 69 5.0 692 2 H71494 probable thiol-dis
911 69 5.0 702 2 T13505 NADH2 dehydrogenas
912 69 5.0 724 2 B83342 hypothetical prote
913 69 5.0 737 2 T12193 NADH2 dehydrogenas
914 69 5.0 777 2 AF2410 serine/threonine k
915 69 5.0 903 2 AI0015 maltose regulon po
916 69 5.0 904 2 A84212 hypothetical prote
917 69 5.0 975 2 T22788 hypothetical prote
918 68.5 4.9 179 2 AD2573 hypothetical prote
919 68.5 4.9 212 2 AE1473 probable membrane
920 68.5 4.9 278 2 T11550 protein R06C1.2 [i
921 68.5 4.9 289 2 D87933 probable plasma me
922 68.5 4.9 295 2 E69025 conserved hypothet
923 68.5 4.9 296 2 E69025 cation transport p
924 68.5 4.9 303 2 AG1396 conserved hypothet
925 68.5 4.9 305 2 S66005 probable oligopept
926 68.5 4.9 313 2 C71545 NADH2 dehydrogenas
927 68.5 4.9 333 2 S52960 transmembrane pore
928 68.5 4.9 336 2 I64096 hypothetical prote
929 68.5 4.9 346 2 B98135 hypothetical prote
930 68.5 4.9 346 2 AI3152 hypothetical prote
931 68.5 4.9 347 2 G96741 unknown protein Fl
932 68.5 4.9 352 2 T23962 hypothetical prote
933 68.5 4.9 365 2 C97088 spore germination
934 68.5 4.9 367 2 T14228 NADH2 dehydrogenas
935 68.5 4.9 372 2 AB0276 probable membrane
936 68.5 4.9 383 2 C83436 probable MFS metab
937 68.5 4.9 401 2 G95968 probable transport
938 68.5 4.9 407 2 A69188 ammonium transport
939 68.5 4.9 454 2 AE1244 acetyl-CoA carboxy
940 68.5 4.9 454 2 AI1606 acetyl-CoA carboxy
941 68.5 4.9 455 2 F97065 D-xylose-proton sy
942 68.5 4.9 459 2 B95009 potassium uptake p
943 68.5 4.9 459 2 F97880 hypothetical prote
944 68.5 4.9 462 2 H81952 probable integral
945 68.5 4.9 468 2 AF2163 hypothetical prote
946 68.5 4.9 475 2 C83452 cytochrome-c oxida
947 68.5 4.9 487 2 E97747 NADH2 dehydrogenas
948 68.5 4.9 488 1 QXASBI mRNA maturase bil
949 68.5 4.9 489 2 E89102 protein F25E5.11 [i
950 68.5 4.9 507 2 B69316 DNA gyrase, subuni
951 68.5 4.9 509 2 T41034 probable WD-domain
952 68.5 4.9 537 2 AI1277 probable transport
953 68.5 4.9 546 2 G86440 hypothetical prote
954 68.5 4.9 597 2 T41501 major facilitator
955 68.5 4.9 616 2 F90371 amino acid transpo
956 68.5 4.9 627 2 C96981 ABC transporter AT
957 68.5 4.9 637 2 AC3217 potassium uptake p
958 68.5 4.9 685 2 T12129 NADH2 dehydrogenas
959 68.5 4.9 687 2 T12126 NADH2 dehydrogenas
960 68.5 4.9 688 2 T13242 NADH2 dehydrogenas
961 68.5 4.9 688 2 T13373 NADH2 dehydrogenas
962 68.5 4.9 689 2 T13681 NADH2 dehydrogenas
963 68.5 4.9 698 2 T13492 NADH2 dehydrogenas
964 68.5 4.9 701 2 F70155 Na+/H+ antiporter
965 68.5 4.9 716 2 E82016 probable integral
966 68.5 4.9 721 2 B83820 hypothetical prote
967 68.5 4.9 736 2 T12225 NADH2 dehydrogenas
968 68.5 4.9 736 2 T12222 NADH2 dehydrogenas
969 68.5 4.9 741 2 T12711 NADH2 dehydrogenas
970 68.5 4.9 741 2 T12620 NADH2 dehydrogenas
971 68.5 4.9 741 2 T12699 NADH2 dehydrogenas
972 68.5 4.9 743 2 T13700 NADH2 dehydrogenas
973 68.5 4.9 743 2 T12760 NADH2 dehydrogenas
974 68.5 4.9 744 2 T12705 NADH2 dehydrogenas
975 68.5 4.9 745 2 G84995 vacB protein limpo
976 68.5 4.9 746 2 C95110 competence protein
977 68.5 4.9 747 2 T13683 NADH2 dehydrogenas
978 68.5 4.9 750 2 B90137 sulfate permease [

979	68.5	4.9	820	2	D71471	probable DNA misma	1052	68	4.9	899	2	S76449	hypothetical prote
980	68.5	4.9	827	2	A95877	hypothetical prote	1053	68	4.9	906	2	S35342	Golgi-associated p
981	68.5	4.9	870	2	A89201	protein F32D8.4 [i	1054	68	4.9	999	2	F72453	probable cytochrom
982	68.5	4.9	874	2	JQ0883	genome polyprotein	1055	68	4.9	1039	2	C87083	C-term lysyl-tRNA
983	68.5	4.9	881	2	AE2777	potassium efflux s	1056	68	4.9	1082	2	T45096	probable arabinosy
984	68.5	4.9	881	2	B97557	hypothetical prote	1057	68	4.9	1323	2	T18214	ATP binding casses
985	68.5	4.9	912	2	T21659	hypothetical prote	1058	68	4.9	1368	2	T51622	probable aldehyde
986	68.5	4.9	960	2	A82142	probable cell divi	1059	68	4.9	1541	1	S71839	canalicular multid
987	68.5	4.9	1081	2	T52028	cellulose synthase	1060	67.5	4.8	100	2	B69836	hypothetical prote
988	68.5	4.9	1084	2	T08583	cellulose synthase	1061	67.5	4.8	212	2	A11111	hypothetical prote
989	68.5	4.9	1394	2	S66876	ATP-dependent tran	1062	67.5	4.8	269	2	E72693	hypothetical prote
990	68.5	4.9	1504	2	A33602	DNA-directed DNA p	1063	67.5	4.8	284	2	AC1198	Streptococcus agal
991	68	4.9	148	2	S74589	hypothetical prote	1064	67.5	4.8	288	2	T33224	hypothetical prote
992	68	4.9	183	2	T49855	hypothetical prote	1065	67.5	4.8	291	2	B95316	probable ABC trans
993	68	4.9	214	2	G83882	hypothetical prote	1066	67.5	4.8	293	2	D81673	ABC transporter, p
994	68	4.9	215	2	S16564	nolH protein - Rhi	1067	67.5	4.8	300	2	G70943	hypothetical prote
995	68	4.9	237	2	H86841	transport permease	1068	67.5	4.8	302	2	G90078	hypothetical prote
996	68	4.9	241	2	T33804	hypothetical prote	1069	67.5	4.8	302	2	G71660	hypothetical prote
997	68	4.9	252	2	A70529	hypothetical prote	1070	67.5	4.8	302	2	AF2686	ABC transporter, m
998	68	4.9	254	2	E70438	type 4 prepilin pe	1071	67.5	4.8	302	2	C97468	probable permease
999	68	4.9	256	2	C72261	spermidine/putresc	1072	67.5	4.8	304	2	AD1029	probable membrane
1000	68	4.9	265	2	AD0214	PTS system, mannos	1073	67.5	4.8	307	2	C70952	probable suga prot
1001	68	4.9	265	2	E82716	ATP synthase, A ch	1074	67.5	4.8	310	2	A86812	sugar ABC transpor
1002	68	4.9	282	2	AD0848	Iron transport pro	1075	67.5	4.8	314	2	AB2230	hypothetical prote
1003	68	4.9	286	2	D83914	chloramphenicol re	1076	67.5	4.8	323	2	T31828	hypothetical prote
1004	68	4.9	296	2	AD0956	phosphate transpor	1077	67.5	4.8	327	1	S45529	NADPH2:quinone red
1005	68	4.9	304	2	A89905	hypothetical prote	1078	67.5	4.8	327	2	S67168	probable membrane
1006	68	4.9	312	2	F70044	hypothetical prote	1079	67.5	4.8	344	2	T32600	hypothetical prote
1007	68	4.9	316	2	S50336	NADH2 dehydrogenas	1080	67.5	4.8	347	2	T28733	hypothetical prote
1008	68	4.9	316	2	E81321	probable cation tr	1081	67.5	4.8	349	2	S51267	probable galactosy
1009	68	4.9	329	2	F98334	SN-glycerol 3-phos	1082	67.5	4.8	359	2	I51372	angiotensin II rec
1010	68	4.9	335	2	S44635	f22b7.7 protein -	1083	67.5	4.8	361	2	D72384	conserved hypothet
1011	68	4.9	353	2	T06515	probable adenosylm	1084	67.5	4.8	364	1	S77360	cbiD protein - Syn
1012	68	4.9	357	2	C97744	hypothetical prote	1085	67.5	4.8	367	2	T23290	hypothetical prote
1013	68	4.9	358	2	T38914	para-hydroxybenzoa	1086	67.5	4.8	374	2	C91198	BspD protein [impo
1014	68	4.9	396	2	AF0677	probable membrane	1087	67.5	4.8	374	2	G86044	secreted protein E
1015	68	4.9	396	2	A91019	probable antibioti	1088	67.5	4.8	377	2	T21170	hypothetical prote
1016	68	4.9	396	2	C85863	probable antibioti	1089	67.5	4.8	379	2	D81515	cell shape-determi
1017	68	4.9	397	2	G90013	hypothetical prote	1090	67.5	4.8	387	2	JE0364	lactosylceramide a
1018	68	4.9	408	2	AC1373	conserved hypothet	1091	67.5	4.8	393	2	T12608	NADH2 dehydrogenas
1019	68	4.9	417	2	E82966	tryptophan permeas	1092	67.5	4.8	402	2	B69843	conserved hypothet
1020	68	4.9	437	1	F64614	conserved hypothet	1093	67.5	4.8	409	2	AF3271	probable allantoin
1021	68	4.9	442	2	H81402	probable integral	1094	67.5	4.8	415	2	F91209	low affinity trypt
1022	68	4.9	448	2	G70172	conserved hypothet	1095	67.5	4.8	415	2	A86056	low affinity trypt
1023	68	4.9	461	2	H82186	probable multidrug	1096	67.5	4.8	415	2	A86059	rod shape protein
1024	68	4.9	469	2	C69628	gamma-aminobutyrat	1097	67.5	4.8	415	2	C72026	rod shape protein
1025	68	4.9	476	2	D83600	probable aldehyde	1098	67.5	4.8	415	2	H71841	hypothetical prote
1026	68	4.9	485	2	T24115	hypothetical prote	1099	67.5	4.8	426	2	A96000	probable C4-dicarb
1027	68	4.9	488	1	QXASM4	NADH2 dehydrogenas	1100	67.5	4.8	456	2	B83391	probable amino aci
1028	68	4.9	489	2	B53153	glucose transport	1101	67.5	4.8	456	2	E83750	gluconate permease
1029	68	4.9	494	2	JC2382	sodium/proline sym	1102	67.5	4.8	459	2	S47879	NADH2 dehydrogenas
1030	68	4.9	505	2	B97747	NADH2 dehydrogenas	1103	67.5	4.8	462	2	D81010	conserved hypothet
1031	68	4.9	512	2	G90399	amino acid transpo	1104	67.5	4.8	463	2	A69905	conserved hypothet
1032	68	4.9	521	2	E64181	probable cytochrom	1105	67.5	4.8	463	2	E83242	probable adenylate
1033	68	4.9	523	2	T12198	sucrose transport	1106	67.5	4.8	467	2	AB2493	hypothetical prote
1034	68	4.9	534	2	S64593	probable membrane	1107	67.5	4.8	467	2	A81263	probable integral
1035	68	4.9	537	2	AH1640	probable transport	1108	67.5	4.8	477	2	D83617	probable amino aci
1036	68	4.9	550	2	T37519	probable amino aci	1109	67.5	4.8	483	2	A10449	protein-Npi-phosph
1037	68	4.9	564	2	C83742	cytochrome c oxida	1110	67.5	4.8	486	2	F71683	NADH2 dehydrogenas
1038	68	4.9	592	2	E70488	cytochrome-c oxida	1111	67.5	4.8	490	2	E82740	C4-dicarboxylate t
1039	68	4.9	593	2	S26696	alkaline proteinas	1112	67.5	4.8	495	2	B81297	sodium/proline sym
1040	68	4.9	600	2	C69371	conserved hypothet	1113	67.5	4.8	501	2	T02134	hypothetical prote
1041	68	4.9	602	2	T13679	NADH2 dehydrogenas	1114	67.5	4.8	510	2	H87320	conserved hypothet
1042	68	4.9	617	2	F82744	ferrous iron trans	1115	67.5	4.8	512	2	S28663	cytochrome-c oxida
1043	68	4.9	633	2	I58140	glycine transporte	1116	67.5	4.8	513	2	I45456	NADH2 dehydrogenas
1044	68	4.9	633	2	S45877	uracil transport p	1117	67.5	4.8	514	2	T46131	4-coumarate-CoA li
1045	68	4.9	638	2	JH0673	glycine transport	1118	67.5	4.8	519	1	S02153	NADH2 dehydrogenas
1046	68	4.9	683	2	T12295	NADH2 dehydrogenas	1119	67.5	4.8	552	2	E70731	probable pitB prot
1047	68	4.9	688	2	T13278	NADH2 dehydrogenas	1120	67.5	4.8	560	2	F81423	L-lactate permease
1048	68	4.9	689	2	T13762	NADH2 dehydrogenas	1121	67.5	4.8	568	2	JC7911	Na+-coupled citrat
1049	68	4.9	705	2	T12152	NADH2 dehydrogenas	1122	67.5	4.8	615	2	H82635	hypothetical prote
1050	68	4.9	709	2	A97218	uncharacterized co	1123	67.5	4.8	617	2	B82285	protein-export mem
1051	68	4.9	811	2	T36581	probable transmemb	1124	67.5	4.8	631	2	H70754	probable abc trans

1125	67.5	4.8	637	2	JH0674	L-proline transpor
1126	67.5	4.8	645	2	T12159	NADH2 dehydrogenas
1127	67.5	4.8	645	2	A75390	NADH2 dehydrogenas
1128	67.5	4.8	659	2	T33557	hypothetical prote
1129	67.5	4.8	690	2	D75487	v-type ATP synthas
1130	67.5	4.8	699	2	T12169	NADH2 dehydrogenas
1131	67.5	4.8	703	2	T13074	NADH2 dehydrogenas
1132	67.5	4.8	741	2	T13404	NADH2 dehydrogenas
1133	67.5	4.8	741	2	T13760	NADH2 dehydrogenas
1134	67.5	4.8	741	2	T13776	NADH2 dehydrogenas
1135	67.5	4.8	741	2	T12762	NADH2 dehydrogenas
1136	67.5	4.8	744	2	T12694	NADH2 dehydrogenas
1137	67.5	4.8	744	2	T12611	NADH2 dehydrogenas
1138	67.5	4.8	801	2	A89862	Na+/H+ antiporter
1139	67.5	4.8	812	2	T19446	hypothetical prote
1140	67.5	4.8	820	2	G82168	trimethylamine-N-o
1141	67.5	4.8	823	2	S44873	ZC21.2 protein - C
1142	67.5	4.8	823	2	B81282	probable integral
1143	67.5	4.8	890	2	H69877	calcium-transporti
1144	67.5	4.8	900	2	D97351	sensor protein Kdp
1145	67.5	4.8	936	2	B64567	cytochrome c bioge
1146	67.5	4.8	952	2	T32836	hypothetical prote
1147	67.5	4.8	1199	1	S76549	transcription-repa
1148	67.5	4.8	1247	1	VHWVN2	structural polypro
1149	67.5	4.8	1517	1	F65112	glutamate synthase
1150	67.5	4.8	1517	2	F85985	glutamate synthase
1151	67.5	4.8	1517	2	C91140	glutamate synthase
1152	67.5	4.8	1704	2	T42749	ATP-binding casset
1153	67.5	4.8	1767	2	S60124	transport protein
1154	67.5	4.8	1778	2	AF1116	internalin protein
1155	67.5	4.8	2701	2	S17796	inositol-trisphosp
1156	67	4.8	90	2	E82861	conjugal transfer
1157	67	4.8	109	2	C98018	crcB protein limpo
1158	67	4.8	168	2	A72226	conserved hypothet
1159	67	4.8	180	2	C86290	hypothetical prote
1160	67	4.8	187	2	A95143	membrane protein {
1161	67	4.8	187	2	G98010	conserved hypothet
1162	67	4.8	226	2	S57521	probable arsenical
1163	67	4.8	232	1	G64591	conserved hypothet
1164	67	4.8	259	2	S59152	cytochrome-c oxida
1165	67	4.8	260	2	A91138	hypothetical prote
1166	67	4.8	260	2	D65110	hypothetical 27.9
1167	67	4.8	260	2	D85983	hypothetical prote
1168	67	4.8	261	2	T11826	cytochrome-c oxida
1169	67	4.8	265	2	T05668	pollen allergen ho
1170	67	4.8	268	2	C86944	probable cation-ef
1171	67	4.8	278	2	A99349	bacitracin resista
1172	67	4.8	285	2	A84224	cytochrome c oxida
1173	67	4.8	287	2	B89936	hypothetical prote
1174	67	4.8	288	2	I78556	membrane glycoprot
1175	67	4.8	291	2	S48977	hypothetical prote
1176	67	4.8	293	2	D86065	glucose-1-phosphat
1177	67	4.8	293	2	B91219	glucose-1-phosphat
1178	67	4.8	293	2	H65182	glucose-1-phosphat
1179	67	4.8	308	2	H64409	hypothetical prote
1180	67	4.8	313	2	T24994	hypothetical prote
1181	67	4.8	313	2	C95247	conserved hypothet
1182	67	4.8	313	2	H98111	conserved hypothet
1183	67	4.8	314	2	F81699	peptide ABC transp
1184	67	4.8	323	2	AB0427	octaprenyl-diphosp
1185	67	4.8	328	2	D72566	hypothetical prote
1186	67	4.8	349	2	AD0990	probable membrane
1187	67	4.8	354	2	C82038	nitrogen regulatio
1188	67	4.8	356	2	B84749	hypothetical prote
1189	67	4.8	364	2	T24418	hypothetical prote
1190	67	4.8	364	2	T45253	probable antiporte
1191	67	4.8	367	2	S23349	hypothetical prote
1192	67	4.8	371	2	D97790	octaprenyl-diphosp
1193	67	4.8	377	2	B71699	cell division prot
1194	67	4.8	388	2	B64459	Na+/H+-exchanging
1195	67	4.8	394	2	AH0020	conserved integral
1196	67	4.8	397	2	B70763	probable membrane
1197	67	4.8	401	2	H82175	multidrug resistan

1198	67	4.8	406	2	H89006	protein T22F3.11 [
1199	67	4.8	407	2	AD0706	O-antigen polymera
1200	67	4.8	407	2	A43672	O-antigen polymera
1201	67	4.8	409	2	C82644	transcription regu
1202	67	4.8	411	2	S61245	probable virion gl
1203	67	4.8	416	2	JN0720	glucosyl transfera
1204	67	4.8	417	2	H83708	hypothetical prote
1205	67	4.8	421	2	AF2382	hypothetical prote
1206	67	4.8	423	2	E82611	conserved hypothet
1207	67	4.8	430	2	S74039	hypothetical prote
1208	67	4.8	446	2	AC3349	protein translocas
1209	67	4.8	453	2	A43765	stsl+ protein - fi
1210	67	4.8	453	2	T30985	hypothetical prote
1211	67	4.8	456	2	AI2789	manganese transpor
1212	67	4.8	458	2	H71657	NADH2 dehydrogenas
1213	67	4.8	459	1	DNHUN4	NADH2 dehydrogenas
1214	67	4.8	461	2	H97568	manganese transpor
1215	67	4.8	462	2	T34365	hypothetical prote
1216	67	4.8	468	2	AD0521	probable symporter
1217	67	4.8	469	2	T35670	hypothetical prote
1218	67	4.8	470	2	T26602	hypothetical prote
1219	67	4.8	473	2	AG0612	probable transport
1220	67	4.8	477	2	S71323	alpha-1A adrenergi
1221	67	4.8	485	2	C70488	cytochrome-c oxida
1222	67	4.8	491	2	G69251	proline permease (
1223	67	4.8	494	2	AC0133	probable permease
1224	67	4.8	511	2	H90439	hypothetical prote
1225	67	4.8	516	2	T33269	hypothetical prote
1226	67	4.8	517	2	AC2070	Na+/H+ antiporter
1227	67	4.8	517	2	E82147	hypothetical prote
1228	67	4.8	522	2	F86215	protein T6D22.18 [
1229	67	4.8	527	2	T49241	pectinesterase-lik
1230	67	4.8	537	2	D70478	conserved hypothet
1231	67	4.8	546	2	AE0571	probable membrane
1232	67	4.8	557	2	T46520	probable transmemb
1233	67	4.8	557	2	S58688	probable transport
1234	67	4.8	557	2	G69096	hypothetical prote
1235	67	4.8	574	2	T41068	hypothetical prote
1236	67	4.8	574	2	T34208	hypothetical prote
1237	67	4.8	584	2	B82810	ABC transporter ni
1238	67	4.8	605	2	A36361	glucose transport
1239	67	4.8	625	2	T33792	hypothetical prote
1240	67	4.8	625	2	AD2251	two-component sens
1241	67	4.8	640	2	D90174	hypothetical prote
1242	67	4.8	644	2	S44478	NADH2 dehydrogenas
1243	67	4.8	653	2	T19245	hypothetical prote
1244	67	4.8	659	2	C65022	yffG protein - Esc
1245	67	4.8	698	2	T12586	NADH2 dehydrogenas
1246	67	4.8	698	2	T12568	NADH2 dehydrogenas
1247	67	4.8	698	2	S76532	hypothetical prote
1248	67	4.8	699	2	T13778	NADH2 dehydrogenas
1249	67	4.8	707	2	G86894	hypothetical prote
1250	67	4.8	741	1	S34218	1,4-alpha-glucan b
1251	67	4.8	741	2	T13764	NADH2 dehydrogenas
1252	67	4.8	878	2	A87385	TonB-dependent rec
1253	67	4.8	918	2	A44257	interleukin-6 sign
1254	67	4.8	970	2	F64230	spore germination
1255	67	4.8	1001	2	T13807	potassium channel
1256	67	4.8	1218	2	S38182	probable transport
1257	67	4.8	1440	2	JC6312	protein-tyrosine-p
1258	67	4.8	1457	1	A48066	protein-tyrosine-p
1259	67	4.8	1489	2	S73015	polyketide synthas
1260	67	4.8	1559	2	AI2348	ferredoxin-glutama
1261	67	4.8	1758	2	F88559	protein C48B4.4b [
1262	67	4.8	2183	2	S47307	genome polyprotein
1263	66.5	4.8	175	2	A95058	conserved domain p
1264	66.5	4.8	175	2	B97927	hypothetical prote
1265	66.5	4.8	185	2	D81327	probable integral
1266	66.5	4.8	205	2	A87460	DedA family protei
1267	66.5	4.8	217	2	B69396	hypothetical prote
1268	66.5	4.8	245	2	F71887	hypothetical prote
1269	66.5	4.8	256	2	G82804	phosphatidyltransf
1270	66.5	4.8	258	2	A69830	hypothetical prote

1271 66.5 4.8 261 2 I64249 hypothetical prote
1272 66.5 4.8 269 2 A86889 zinc ABC transport
1273 66.5 4.8 279 2 E69226 hypothetical prote
1274 66.5 4.8 292 2 A70546 probable menA prot
1275 66.5 4.8 292 2 F83823 hypothetical prote
1276 66.5 4.8 293 2 T41928 hypothetical prote
1277 66.5 4.8 295 2 AE0993 glycerol-3-phospha
1278 66.5 4.8 306 2 C70141 oligopeptide ABC t
1279 66.5 4.8 306 2 S55047 ABC-type transport
1280 66.5 4.8 320 2 T23635 hypothetical prote
1281 66.5 4.8 361 2 T37938 hypothetical prote
1282 66.5 4.8 366 2 G95376 conserved hypothet
1283 66.5 4.8 375 2 T05707 phosphate transpor
1284 66.5 4.8 385 2 B87441 rod shape-determin
1285 66.5 4.8 389 2 ADi378 cell division prot
1286 66.5 4.8 390 2 AH0260 conserved hypothet
1287 66.5 4.8 394 2 T13721 NADH2 dehydrogenas
1288 66.5 4.8 405 2 T40193 hypothetical prote
1289 66.5 4.8 409 2 B85735 probable membrane
1290 66.5 4.8 410 2 E75290 probable multidrug
1291 66.5 4.8 411 2 S73218 preprotein translo
1292 66.5 4.8 421 2 E90883 hypothetical prote
1293 66.5 4.8 422 2 H69839 multidrug resistan
1294 66.5 4.8 428 2 G82918 hypothetical prote
1295 66.5 4.8 438 2 H91112 hypothetical prote
1296 66.5 4.8 438 2 H85957 partial probable t
1297 66.5 4.8 440 2 C71863 probable aminotran
1298 66.5 4.8 441 2 T19306 hypothetical prote
1299 66.5 4.8 452 2 D86835 maltose ABC transp
1300 66.5 4.8 454 2 A70079 conserved hypothet
1301 66.5 4.8 467 2 F90544 conserved hypothet
1302 66.5 4.8 467 2 T16319 hypothetical prote
1303 66.5 4.8 469 2 H70626 probable narK3 pro
1304 66.5 4.8 471 2 F71543 probable dicarboxy
1305 66.5 4.8 472 2 E83497 probable amino aci
1306 66.5 4.8 474 2 S07754 NADH2 dehydrogenas
1307 66.5 4.8 475 2 T46745 arginine/ornithine
1308 66.5 4.8 478 2 D64895 probable membrane
1309 66.5 4.8 480 2 D90038 PTS system, sucros
1310 66.5 4.8 484 2 E75138 osmoregulated prol
1311 66.5 4.8 491 2 H84379 4-hydroxybutyrate
1312 66.5 4.8 492 2 T15603 hypothetical prote
1313 66.5 4.8 498 2 AI0482 phosphate transpor
1314 66.5 4.8 499 2 A65085 probable low-affin
1315 66.5 4.8 509 2 T11043 cytochrome-c oxida
1316 66.5 4.8 513 2 T14864 probable monosacch
1317 66.5 4.8 513 2 C81859 probable integral
1318 66.5 4.8 519 2 E90548 conserved hypothet
1319 66.5 4.8 520 2 D90014 hypothetical prote
1320 66.5 4.8 526 2 H85891 hydrogenase 4 memb
1321 66.5 4.8 526 2 E65024 Hydrogenase-4 comp
1322 66.5 4.8 530 2 T11884 cytochrome-c oxida
1323 66.5 4.8 553 2 T38541 probable sucrose c
1324 66.5 4.8 557 2 T49811 probable vacuolar
1325 66.5 4.8 569 2 T37706 probable sodium/hy
1326 66.5 4.8 573 2 T23102 hypothetical prote
1327 66.5 4.8 574 2 G84578 probable potassium
1328 66.5 4.8 648 2 C97961 DNA topoisomerase
1329 66.5 4.8 648 2 F95093 DNA gyrase chain B
1330 66.5 4.8 649 2 AB2154 hypothetical prote
1331 66.5 4.8 659 2 S67175 probable membrane
1332 66.5 4.8 660 1 S54746 cytochrome c-type
1333 66.5 4.8 664 2 B53610 ntpti protein - Ent
1334 66.5 4.8 679 2 H95036 glycosyl hydrolase
1335 66.5 4.8 699 2 T12173 NADH2 dehydrogenas
1336 66.5 4.8 703 2 H86588 thio-disulfide int
1337 66.5 4.8 703 2 H72034 thiol-disulfide in
1338 66.5 4.8 714 2 G81503 thiol-disulfide in
1339 66.5 4.8 725 2 S52990 phenylalanine ammo
1340 66.5 4.8 732 2 AD0014 primosomal protein
1341 66.5 4.8 737 2 D97907 alpha-xylosidase (
1342 66.5 4.8 741 2 T12605 NADH2 dehydrogenas
1343 66.5 4.8 741 2 T13361 NADH2 dehydrogenas

1344 66.5 4.8 744 2 T13063 NADH2 dehydrogenas
1345 66.5 4.8 744 2 T13048 NADH2 dehydrogenas
1346 66.5 4.8 746 2 T01536 hypothetical prote
1347 66.5 4.8 755 2 T20950 hypothetical prote
1348 66.5 4.8 759 2 D70422 cellulose synthase
1349 66.5 4.8 790 2 G90477 hypothetical prote
1350 66.5 4.8 812 2 T16621 hypothetical prote
1351 66.5 4.8 820 2 T41978 helicase - human h
1352 66.5 4.8 860 2 C82750 mannosyltransferas
1353 66.5 4.8 919 2 S19810 glutamate receptor
1354 66.5 4.8 919 2 I53474 kainate receptor -
1355 66.5 4.8 937 2 T37241 olfactory channel
1356 66.5 4.8 957 2 D88651 protein B0212.5 li
1357 66.5 4.8 999 2 T27628 hypothetical prote
1358 66.5 4.8 1002 2 G97217 conserved membrane
1359 66.5 4.8 1010 1 PXZP2P H+-exporting ATPas
1360 66.5 4.8 1049 2 T22762 hypothetical prote
1361 66.5 4.8 1068 2 AB1082 B. subtilis YueB p
1362 66.5 4.8 1088 2 H84604 probable cellulose
1363 66.5 4.8 1248 2 C89874 autolysin [importe
1364 66.5 4.8 1704 2 A59188 ATP-binding casset
1365 66.5 4.8 1704 2 S71363 probable ATP-bindi
1366 66 4.7 101 2 G69894 hypothetical prote
1367 66 4.7 105 2 AH2209 hypothetical prote
1368 66 4.7 158 2 S58016 probable olfactory
1369 66 4.7 171 2 S44146 amis protein - Pee
1370 66 4.7 172 2 A83226 alpha-crystallin c
1371 66 4.7 195 1 CYHYAM hypothetical prote
1372 66 4.7 196 2 AD2304 hypothetical prote
1373 66 4.7 203 2 T05519 hypothetical prote
1374 66 4.7 203 2 C85288 hypothetical prote
1375 66 4.7 204 2 D69097 hypothetical prote
1376 66 4.7 211 2 E89963 hypothetical prote
1377 66 4.7 255 2 AH0577 molybdopterin-cont
1378 66 4.7 256 2 JQ1106 tonoplast intrinsi
1379 66 4.7 260 2 AG0904 probable ABC transp
1380 66 4.7 265 2 H90254 conserved membrane
1381 66 4.7 267 2 A87233 NosY protein PA339
1382 66 4.7 275 2 F83222 hema concentration
1383 66 4.7 276 2 F75057 hypothetical prote
1384 66 4.7 280 2 S44085 plasma membrane in
1385 66 4.7 285 2 E84789 hypothetical prote
1386 66 4.7 285 2 E84789 hypothetical prote
1387 66 4.7 285 2 D84789 hypothetical prote
1388 66 4.7 295 2 G72760 NADH2 dehydrogenas
1389 66 4.7 298 2 T13684 cation transport p
1390 66 4.7 303 2 AB1772 hypothetical prote
1391 66 4.7 307 2 T16457 permease [importe
1392 66 4.7 311 2 AI2697 hypothetical prote
1393 66 4.7 311 2 B97480 branched-chain ami
1394 66 4.7 312 2 G69423 hypothetical prote
1395 66 4.7 312 2 H90517 hypothetical prote
1396 66 4.7 318 2 AI1811 hypothetical prote
1397 66 4.7 320 2 T25308 NADH2 dehydrogenas
1398 66 4.7 322 2 T13486 conserved hypothet
1399 66 4.7 330 1 H69798 hypothetical prote
1400 66 4.7 335 2 T39425 hypothetical prote
1401 66 4.7 336 2 T31762 hypothetical prote
1402 66 4.7 344 2 AB3236 NADH2 dehydrogenas
1403 66 4.7 354 2 S70595 conserved hypothet
1404 66 4.7 355 2 A64138 hypothetical prote
1405 66 4.7 357 2 T03557 rfe protein - Haem
1406 66 4.7 357 2 F81916 ribose transport s
1407 66 4.7 371 2 AD1201 probable integral
1408 66 4.7 377 2 H64387 N-acyl-L-amino aci
1409 66 4.7 381 2 C71680 hypothetical prote
1410 66 4.7 383 2 E87680 hypothetical prote
1411 66 4.7 395 2 A86527 neutral amino acid
1412 66 4.7 395 2 E72095 neutral amino acid
1413 66 4.7 396 2 AH2859 MFS permease [impo
1414 66 4.7 396 2 F97636 probable transport
1415 66 4.7 398 2 H75043 mg2+ transport pro
1416 66 4.7 404 2 S65991 membrane protein y

Db 848 FAIIAAMVAWALIRNLPGLLEVLVLSRLNMRQASAYAITILNVYIIAVGAMTVFGSLGV 907

Qy 103 -----CLGLSIVANFQKTTLFAAHVSGAVLTF-----GMGSLYMF 137

Db 908 SWDKLQWLAAALSGLGFLQEIFGNEFVSGLIILFERPVRIGDVTVTIGTYSGTVSKIRIR 967

Qy 138 VQTILSYQMPKIHGKQVFWIRLLLVICWGSALSMLTCSVLHSG-NFGTDLEQKLHWN 196

Db 968 ATTITDFDRKEVVIIPNKAFLVTERLINW-----SLSDTTTTRLVIRLGAVAYGSDLEK----- 1017

Qy 197 PEDKGYVLHMITTAA-----EWSMSFSFFGF-----FLTYIRDFQKISLRVE 238

Db 1018 -----VKRVLQAAAMEHPKVMHDEPAVFFTTFGASTLDHELRLYVRELDRSHTVD 1069

RESULT 6

E72523

carbon starvation protein A homolog APE2162 [similarity] - Aeropyrum pernix (strain Kl)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: E72523

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: E72523

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-604 <KAW>

A;Cross-references: UNIPROT:Q9Y9X7; DDBJ:AP000063; NID:g5105654; PIDN:BAA81173.1; PID:g5

A;Experimental source: strain Kl

C;Genetics:

A;Gene: APE2162

C;Superfamily: carbon starvation protein

Query Match 7.0%; Score 97; DB 2; Length 604;

Best Local Similarity 23.9%; Pred. No. 1.1;

Matches 69; Conservative 39; Mismatches 101; Indels 80; Gaps 16;

Qy 4 FQOGLSFLPSAL--VIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLN 61

Db 183 YRMGLGMPSTVITVVLVIAAFVSYNHGIVIGTFDPSLP-PGEGGWAYHRWVI--ILG 239

Qy 62 IAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVLSCLGLSIVANFQKTTLFAAH 121

Db 240 LYALLA-ASLPVWY----LLQPRD---YLNAYILWTG---LGLAAIA---AILLGTQS 283

Qy 122 VSGAVLTFMGSLYMFVQTILSYQMPKIHGKQVFWIRLLLVICWGSALSMLTCSVLH 181

Db 284 LKGPAYT-----SFQPNIIAGQTFP-----FWPAIPLIIACG---SLSGFHSIVA 325

Qy 182 SGNFGTDLEQKLH-----WN-PE--DKGYV-LHMITTA 210

Db 326 SGTTSKQLASELDALFVGYGAMLLEGALSGLAVIIPISFAWNAPELIQKGVINNMLDLA 385

Qy 211 A-----EWSMSFSFFGFLTYIRDFQKISLRVEANLHGLTLYDT 249

Db 386 AVPRYAVGYGYTLAKTFEMFGVGFDTGYSFFTLFASLMSMYVLTTLDT 434

RESULT 7

S43882

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - garden lettuce mitochondrion

C;Species: mitochondrion Lactuca sativa (garden lettuce)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S43882

R;Geiss, K.T.; Abbas, G.M.; Makaroff, C.A.

Mol. Gen. Genet. 243, 97-105, 1994

A;Title: Intron loss from the NADH dehydrogenase subunit 4 gene of lettuce mitochondrial

A;Reference number: S43882; MUID:94247363; PMID:8190077

A;Accession: S43882

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-495 <GEI>

A;Cross-references: UNIPROT:Q37544

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 96; DB 2; Length 495;

Best Local Similarity 24.6%; Pred. No. 1.1;

Matches 55; Conservative 34; Mismatches 83; Indels 52; Gaps 12;

Qy 8 LSFLEPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62

Db 277 LCFTP---FIYTLSAIAIYTSLTTLRQID--LKKIIAYSSVAHMLNLTIGMFSLNIQGI 331

Qy 63 -----AAVLCIATYVRYKQ-----VHALSPEENVIIKLNKAGLVL 98

Db 332 GGSILLMLSHGLVSSALFLCVGLVYVRHKTRLVRYGGLVSTMPNFSTIFFFTLANMSL 391

Qy 99 -GILSCLG--LSIVANFQKTTLFAAHVSGAVLTFMGSLYMFVQVQVILSYQMP----- 148

Db 392 PGTSSFIGEFLILVGAFORNSLVATLAALGMILGAAYSLWLY-NRVVSGNLKPDFLHKFS 450

Qy 149 KIHGKQVF-WIRLLL-VIWCVSALSMLTLC-----SSVLHSGNF 185

Db 451 DLNGTEVFIFIPFLVGVVMGVYPKVPFPPDCMHTSVSNLVQHCKF 494

RESULT 8

S16447

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - wheat mitochondrion

N;Alternate names: mitochondrial complex I subunit IV

C;Species: mitochondrion Triticum aestivum (common wheat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S16447; S16448; S06835

R;Lamattina, L.; Grienemberger, J.M.

Nucleic Acids Res. 19, 3275-3282, 1991

A;Title: RNA editing of the transcript coding for subunit 4 of NADH dehydrogenase in whe

A;Reference number: S16447; MUID:91288205; PMID:1712098

A;Accession: S16447

A;Molecule type: mRNA

A;Residues: 1-495 <LAM>

A;Cross-references: UNIPROT:P27572; EMBL:X57163

A;Note: the authors translated the codon CGT for residue 418 as Ala

A;Accession: S16448

A;Molecule type: DNA

A;Residues: 1-14,'P',16-24,'TP',27-35,'P',37-51,'PP',54,'PR',57-65,'S',67-105,'S',107-120

'H',474-477,'P',479-495 <LAF>

A;Cross-references: EMBL:X57164; NID:g21823; PIDN:CAA40453.1; PID:g21824

A;Note: the authors translated the codon CGT for residue 418 as Ala

A;Note: 15-P, 25-Thr, 26-Pro, 36-Pro, 52-Pro, 53-Pro, 55-Pro, 56-Arg, 66-Ser, 106-Ser, 1

re due to RNA editing

R;Lamattina, L.; Weil, J.H.; Grienemberger, J.M.

FEBS Lett. 258, 79-83, 1989

A;Title: RNA editing at a splicing site of NADH dehydrogenase subunit IV gene transcript

A;Reference number: S06835; MUID:90076495; PMID:2687023

A;Accession: S06835

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 295-346 <LAW>

C;Genetics:

A;Gene: nad4

A;Genome: mitochondrion

A;Introns: 154/2; 326/1; 467/1

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.8%; Score 94; DB 1; Length 495;

Best Local Similarity 24.1%; Pred. No. 1.7;

Matches 54; Conservative 34; Mismatches 84; Indels 52; Gaps 11;

Qy 8 LSFLEPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAM--LNI--- 62

Db 277 LCFTP---FIYTLSAIAIIYTSLTTLRQID--LKKIIAYSSVAHMNLVTIGMFSLNIQGI 331

QY 63 -----AAVLCIATIVVRYKQ-----VHALSPEENVIIKLNKAGLVL 98

Db 332 GGSILLMLSHGLVSSALFLCVGLYDRHKTRLVRYGGLVSTMPNFSTIFFFTLANMSL 391

QY 99 -GILSCLG--LSIVANFQKTTLFAAHVSGAVLTFMGSLYMFVQTIILSYQMOP----- 148

Db 392 PGTSSFIGEFLILVGAFQRNSLVATLRALGMILGAAYSLWL-VRVVSGLNKPDFLYKFS 450

QY 149 KIHGQVFWIR--LLLVIWCGVSALSMLTLC-----SSVLHSGNF 185

Db 451 DLNGREVFIPLPFLVGVMGMGYPKVFLDCMHTSVSNLVQHGF 494

RESULT 9

D96506

hypothetical protein Tl2C22.2 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: D96506

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzialì, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: D96506

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-379 <STO>

A;Cross-references: UNIPROT:Q9LPF6; GB:AE005173; NID:g8655985; PIDN:AAF78258.1; GSPDB:GN

C;Genetics:

A;Gene: Tl2C22.2

A;Map position: 1

C;Superfamily: Arabidopsis thaliana hypothetical protein T9A21.70

Query Match 6.7%; Score 93.5; DB 2; Length 379;

Best Local Similarity 21.8%; Pred. No. 1.4;

Matches 47; Conservative 53; Mismatches 95; Indels 21; Gaps 9;

QY 10 FLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFG-AMLNIAA---- 64

Db 90 YIP--L LLLPSSASVESSESSCLKYI--VLIYVLLGVIIAGDNMLYSVGLLYLSASTYS 145

QY 65 VLCIATIVVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAAHVSG 124

Db 146 LICATQLAFNAVFSYFINAQFTALILNSVLLSFSAAIALNDADTPSGVSRSKYIVG 205

QY 125 AVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLVWCGVSALSMLTSCSSVLHSGN 184

Db 206 FVCTLAASALYSLLLSLMQFSFE-KILKRETFSVVLEMQIYTSLVA----TCVSVI--GL 258

QY 185 FGTDLEQKLHNPE--DKG---YVLHMITTAAEWSM 215

Db 259 FASGEWRTLHGEMEGYHKGOASVYTLVWTAVTWQV 294

RESULT 10

F71651

putrescine-ornithine antiporter (pote) RP483 - Rickettsia prowazekii

C;Species: Rickettsia prowazekii

C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004

C;Accession: F71651

R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, u Nature 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.

A;Reference number: A71630; MUID:99039499; PMID:9823893

A;Accession: F71651

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-429 <AND>

A;Cross-references: UNIPROT:Q9ZD63; GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAAL493

A;Experimental source: strain Madrid E

C;Genetics:

A;Gene: pote; RP483

C;Superfamily: L-lysine transport protein

Query Match 6.7%; Score 93.5; DB 2; Length 429;

Best Local Similarity 24.1%; Pred. No. 1.6;

Matches 48; Conservative 37; Mismatches 79; Indels 35; Gaps 10;

QY 11 LPSALVIWTSAAFIYSYITAVTLHHIDPA-----LPYISDTGTVAPEKCLFGAMLN-- 61

Db 217 IPRAIIIGTCCVAFLYIINSIGIIGLIPASELINSKAPY-ADAATL-----LFGGTWSKV 270

QY 62 ---IAAVLCIATI---YVRYKQVHALSPEENVIIKL-----NKAGLVGLSCLGLSIV 109

Db 271 ITVIASVICIGTLNAWVLTSQIALGLAEDGLLPKFFAKKNSNNAPTYGIIISCLGITPL 330

QY 110 ANFQKTTLFAAHVSGAVLTFMGSLYMFVQTIILSYQMOPKI-HGKQVFWIRLLLVWCGV 168

Db 331 LLFTSNNFAKQIT-QIIDFSV-IAFLFYVILCSLAFCLKVIFSSKENFSYYL-----V 383

QY 169 SALSMLTSCSSVLHSGNFGT 187

Db 384 AIISIIIFTWVIYKTPFET 402

RESULT 11

F90693

mechanosensitive channel protein [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: F90693

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: F90693

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1120 <HAY>

A;Cross-references: UNIPROT:Q8XD54; GB:BA000007; PIDN:BAB33941.1; PID:g13359975; GSPDB:GN

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs0518

Query Match 6.7%; Score 93; DB 2; Length 1120;

Best Local Similarity 19.6%; Pred. No. 5;

Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;

QY 1 MWWFQQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Db 805 MFW-----AIWSDLITVFSYLDISITLWHYNG-----TEAGAAVVKNVTMGSL 847

QY 61 -----NIAAVLCIATIVVRYKQVHALSPEENVIIKLNKAGLVGLS- 102

Db 848 FAIIASMVAWALIRNLPGLLEVLVLSRLNMRQGASYAITILNYIIAIVGAMTVFGSLGV 907

QY 103 -----CLGLSIVANFQKTTLFAAHVSGAVLTF-----GMGSLYMF 137

Db 908 SWDKLQWLAAALSVDGLGFLQEIIFGNFVSLIILFERPVRIGDVTIGSFSGTVSKIR 967

QY 138 VQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTSCSSVLHSG-NFGTDLEQ 191

Db 968 ATTITDFDRKEVIIPNKAF-VTERLINW---SLTDTTTRLVIRLVAGVYGSDDLEK 1017

RESULT 12

B85544
mechanosensitive channel protein [similarity] - Escherichia coli (strain O157:H7, substra
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85544
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: B85544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1120 <STO>
A;Cross-references: UNIPROT:Q8XD54; GB:AE005174; NID:g12513332; PIDN:AAG54814.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: aefa

Query Match 6.7%; Score 93; DB 2; Length 1120;
Best Local Similarity 19.6%; Pred.No. 5;
Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;

QY 1 MWWFQQLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 805 MFW-----AIWSDLITVFSYLDSTITLWHYNG-----TEAGAAVVKNVMTGSL 847
QY 61 -----NIAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVLGILS- 102
Db 848 FAIIASMVAWALIRNLPGLLEVLVLSRLNMRQGASYAITILNYIIIAVGAMTVFGSLGV 907
QY 103 -----CLGLSIVANFQKTTLFAAHVSGAVLTF-----GMGSLYMF 137
Db 908 SWDKLQWLAAALS VGLGFLQEIFGNFVSGLIILFERPVRIGDVTVTIGSPGTVSKIRIR 967
QY 138 VQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSVLSHG-NFGTDLEQ 191
Db 968 ATTITDFRKEVIIPNKA F-VTERLINW-----SLTDTTTRLVIRLGVA YGSDLEK 1017
A;Accession: H64776
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64776
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1120 <BLAT>
A;Cross-references: UNIPROT:P77338; GB:AE000152; GB:U00096; NID:g1786660; PIDN:AAC73567.
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: aefa

RESULT 13
H64776
probable membrane protein aefa - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: H64776
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64776
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1120 <BLAT>
A;Cross-references: UNIPROT:P77338; GB:AE000152; GB:U00096; NID:g1786660; PIDN:AAC73567.
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: aefa
C;Keywords: transmembrane protein
F;12-28/Domain: transmembrane #status predicted <TM1>
F;504-520/Domain: transmembrane #status predicted <TM2>
F;561-577/Domain: transmembrane #status predicted <TM3>
F;630-646/Domain: transmembrane #status predicted <TM4>
F;663-679/Domain: transmembrane #status predicted <TM5>
F;693-709/Domain: transmembrane #status predicted <TM6>
F;793-809/Domain: transmembrane #status predicted <TM7>
F;844-860/Domain: transmembrane #status predicted <TM8>
F;892-908/Domain: transmembrane #status predicted <TM9>

Query Match 6.7%; Score 93; DB 2; Length 1120;
Best Local Similarity 19.6%; Pred.No. 5;
Matches 46; Conservative 38; Mismatches 85; Indels 66; Gaps 8;

QY 1 MWWFQQLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 805 MFW-----AIWSDLITVFSYLDSTITLWHYNG-----TEAGAAVVKNVMTGSL 847
QY 61 -----NIAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVLGILS- 102
Db 848 FAIIASMVAWALIRNLPGLLEVLVLSRLNMRQGASYAITILNYIIIAVGAMTVFGSLGV 907
QY 103 -----CLGLSIVANFQKTTLFAAHVSGAVLTF-----GMGSLYMF 137
Db 908 SWDKLQWLAAALS VGLGFLQEIFGNFVSGLIILFERPVRIGDVTVTIGSPGTVSKIRIR 967
QY 138 VQTILSYQMOPKIHGKQVFWIRLLLVICWGSALSMLTCSVLSHG-NFGTDLEQ 191
Db 968 ATTITDFRKEVIIPNKA F-VTERLINW-----SLTDTTTRLVIRLGVA YGSDLEK 1017

RESULT 14
AE0801
probable amino acid transporter STY2589 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE0801
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0801
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-473 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07591.1; PID:g16503583; GSPDB:GN00176
C;Genetics:
A;Gene: STY2589

Query Match 6.6%; Score 92.5; DB 2; Length 473;
Best Local Similarity 22.8%; Pred.No. 2.1;
Matches 59; Conservative 36; Mismatches 95; Indels 69; Gaps 14;

QY 13 SALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATY 72
Db 37 SALLLVIIAFCCLFFPLAMVCGELSTGWP--KDGIFVWIKEAFGKRIAWIVVVCF---- 90
QY 73 VRYKQVHALSPEENVIIKLNKAGLVGILSC-LGUSIVANFQKTTLFAAHVSGAVLT--- 128
Db 91 -----LFSCVLFPPMLQFGFTAL--GYMIGGGLAENK 121
QY 129 --FGMGSLYMF-VQTILSYQMOPKIHGKQVFWIRLL--LVIWCGV---SALSMLTCSSVL 180
Db 122 AFIGGSAVIFWLLTLMN-----IRGME--WTKIINSISAWCGVFIPSAIILLAVVWL 173
QY 181 HSGN-FGTDLEQKLNWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYI-----RDF 230
Db 174 CTGHQMOTDYTTAKNWIP-DLG---HWDVTIVFLSSMMFAFAGLEVAPMIAGRTRNPORDF 229
QY 231 QKISLRVEANLHGLTLYDT 249
Db 230 PRAMAVSAAVIVGIYVMGT 248

RESULT 15
T24487
hypothetical protein T05A1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24487
R;Lloyd, C.
submitted to the EMBL Data Library, December 1995

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 17:15:16 ; Search time 174 Seconds
(without alignments)
782.834 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
Sequence: 1 MWFFQQLSFLPSALVIWTS.....YDTAPCPINNERTRLISRDI 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues 1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB ID	Description
		Match	Length		
1	1392	100.0	266	Q6UX65	Q6ux65 homo sapien
2	1245	89.4	267	Q9CR48	Q9cr48 m mus muscu
3	1235	88.7	267	Q9D520	Q9d520 mus musculus
4	1078	77.4	208	Q86VD3	Q86vd3 homo sapien
5	805.5	57.9	180	Q9D835	Q9d835 mus musculus
6	764.5	54.9	272	Q6IQI0	Q6iqi0 brachydanio
7	725	52.1	136	Q8NEQ4	Q8nbq4 homo sapien
8	492.5	35.4	238	Q8NB62	Q8nb62 homo sapien
9	479.5	34.4	238	Q9DC58	Q9dc58 mus musculus
10	471.5	33.9	287	Q6NRS6	Q6nrs6 xenopus lae
11	439.5	31.6	238	Q8QGB2	Q8qgb2 oncorhynchu
12	388.5	27.9	282	Q7QE61	Q7qe61 anopheles g
13	361.5	26.0	246	Q77262	O77262 drosophila
14	318.5	22.9	252	Q86F93	Q86f93 schistosoma
15	288	20.7	271	Q93319	Q93319 caenorhabdi
16	262	18.8	238	Q8R218	Q8r218 mus musculus
17	251.5	18.1	181	Q6XHF5	Q6xhf5 drosophila
18	251	18.0	132	Q9NUN1	Q9nun1 homo sapien
19	240	17.2	132	Q78J26	Q78j26 mus musculus
20	203	14.6	249	Q8C8S3	Q8c8s3 mus musculus
21	201.5	14.5	271	Q6GPL4	Q6gpl4 xenopus lae
22	191.5	13.8	257	Q6IQJ3	Q6iqj3 brachydanio
23	185.5	13.3	219	Q6P6P1	Q6p6p1 mus musculus
24	183.5	13.2	294	Q7SXX4	Q7sxx4 brachydanio
25	172.5	12.4	243	Q86IK0	Q86ik0 dictyosteli
26	161.5	11.6	123	Q8C9L9	Q8c9l9 mus musculus
27	160.5	11.5	271	Q86TG1	Q86tgi homo sapien
28	157.5	11.3	271	Q9QZE9	Q9qze9 rattus norv
29	151.5	10.9	271	Q91WN2	Q91wn2 mus musculus
30	150.5	10.8	243	Q86K17	Q86k17 dictyosteli
31	120	8.6	224	Q23135	Q23135 caenorhabdi

105	89.5	6.4	579	2	Q8DZT0	Q8dz0 streptococc	178	86	6.2	233	2	Q662P5	Q662p5 borrelia ga
106	89.5	6.4	579	2	Q8E5H7	Q8e5h7 streptococc	179	86	6.2	234	2	Q8R3W1	Q8r3w1 mus musculu
107	89.5	6.4	599	2	Q22089	Q22089 caenorhabdi	180	86	6.2	372	2	Q6GAU7	Q6gau7 staphylococ
108	89.5	6.4	963	2	Q7R2T8	Q7r2t8 giardia lam	181	86	6.2	373	2	Q99VB1	Q99vb1 staphylococ
109	89	6.4	267	2	Q8BV59	Q8bv59 mus musculu	182	86	6.2	373	2	Q7A6G2	Q7a6g2 staphylococ
110	89	6.4	290	2	Q72YR6	Q72yr6 bacillus ce	183	86	6.2	389	2	Q9V0C0	Q9v0c0 pyrococcus
111	89	6.4	290	2	Q812M6	Q812m6 bacillus ce	184	86	6.2	396	1	BCR_EC0LI	P28246 escherichia
112	89	6.4	428	2	Q66FK2	Q66fk2 yersinia ps	185	86	6.2	444	2	Q7Y8W4	Q7y8w4 portunus tr
113	89	6.4	428	2	Q8ZJ45	Q8zj45 yersinia pe	186	86	6.2	509	2	Q7R5J8	Q7r5j8 giardia lam
114	89	6.4	442	2	Q7MP35	Q7mp35 vibrio vuln	187	86	6.2	667	2	Q8W9Q3	Q8w9q3 mesostigma
115	89	6.4	637	2	Q9H8H9	Q9h8h9 homo sapien	188	86	6.2	701	2	Q8HTM4	Q8htm4 achlys trip
116	89	6.4	659	2	Q7VUY3	Q7vuy3 bordetella	189	86	6.2	703	2	Q9LMM3	Q9lmm3 arabadopsais
117	89	6.4	660	2	Q7WBD6	Q7wbd6 bordetella	190	86	6.2	725	2	P92949	P92949 arabadopsais
118	89	6.4	757	2	Q9UFA2	Q9ufa2 homo sapien	191	86	6.2	841	2	Q93QY7	Q93qy7 staphylococ
119	89	6.4	917	2	Q96FP81	Q96f81 homo sapien	192	86	6.2	954	2	Q7VGA9	Q7vga9 helicobacte
120	89	6.4	917	2	Q9H698	Q9h698 homo sapien	193	86	6.2	1308	2	Q8T6H2	Q8t6h2 dictyosteli
121	88.5	6.4	361	2	Q83F26	Q83f26 coxiella bu	194	85.5	6.1	219	2	Q9CY24	Q9cy24 mus musculu
122	88.5	6.4	430	2	Q9V210	Q9v210 pyrococcus	195	85.5	6.1	219	2	Q9D8L7	Q9d8l7 mus musculu
123	88.5	6.4	680	2	Q9SBY7	Q9sby7 vahlia cape	196	85.5	6.1	250	2	Q6CID8	Q6cid8 kluyveromyc
124	88.5	6.4	691	2	Q8MBV0	Q8mbv0 vahlia cape	197	85.5	6.1	261	2	Q9CP79	Q9cp79 pasteurella
125	88.5	6.4	732	2	Q9TJP3	Q9tjp3 simira viri	198	85.5	6.1	295	2	Q9K0I7	Q9k0i7 neisseria m
126	88.5	6.4	732	2	Q9TJS2	Q9tjs2 pentagonia	199	85.5	6.1	296	2	Q669X3	Q669x3 yersinia ps
127	88.5	6.4	808	2	Q21453	Q21453 caenorhabdi	200	85.5	6.1	296	2	Q8ZF11	Q8zfil yersinia pe
128	88.5	6.4	833	2	Q7USM4	Q7usm4 rhodopirell	201	85.5	6.1	311	1	PAQ3_HUMAN	Q6tch7 homo sapien
129	88	6.3	290	2	Q632P0	Q632p0 bacillus ce	202	85.5	6.1	311	2	Q88TD9	Q88td9 lactobacill
130	88	6.3	290	2	Q81KE4	Q81ke4 bacillus an	203	85.5	6.1	329	2	Q96K55	Q96k55 homo sapien
131	88	6.3	290	2	Q6HC79	Q6hc79 bacillus th	204	85.5	6.1	355	2	Q8TNX8	Q8tnx8 methanosarc
132	88	6.3	372	2	Q8A1P0	Q8a1p0 bacteroides	205	85.5	6.1	399	2	Q75PY5	Q75py5 cavia porce
133	88	6.3	413	2	Q8R792	Q8r792 thermoanaer	206	85.5	6.1	401	2	Q89KV1	Q89kv1 bradyrhizob
134	88	6.3	500	2	Q9TCC1	Q9tcc1 nephroselmi	207	85.5	6.1	458	2	Q8WUB5	Q8wub5 homo sapien
135	88	6.3	546	2	Q8PXP0	Q8pxp0 methanosarc	208	85.5	6.1	498	2	O21287	O21287 reclinomona
136	88	6.3	622	2	Q7S317	Q7s317 neurospora	209	85.5	6.1	526	2	Q90X46	Q90x46 brachydanio
137	88	6.3	660	2	Q7WMV6	Q7wmv6 bordetella	210	85.5	6.1	528	2	Q6A2J4	Q6a2j4 brandisia h
138	88	6.3	661	2	Q74F70	Q74f70 geobacter s	211	85.5	6.1	545	2	Q96JZ5	Q96jz5 homo sapien
139	88	6.3	732	2	Q9TJP1	Q9tjp1 warszewiczi	212	85.5	6.1	587	1	T9S3_MOUSE	Q9et30 mus musculu
140	88	6.3	787	2	Q6SHL0	Q6shl0 uncultured	213	85.5	6.1	589	1	T9S3_HUMAN	Q9hd45 homo sapien
141	88	6.3	929	2	Q9LGC6	Q9lgc6 oryza sativ	214	85.5	6.1	682	2	Q83C62	Q83c62 coxiella bu
142	88	6.3	1165	1	CYA6_CANFA	P30804 canis famil	215	85.5	6.1	696	2	Q9TIW8	Q9tiw8 phacelia ro
143	87.5	6.3	215	2	Q9D2W6	Q9d2w6 mus musculu	216	85.5	6.1	703	2	Q9TLA5	Q9tla5 jasinum me
144	87.5	6.3	233	1	Y117_BORBU	O51144 borrelia bu	217	85.5	6.1	851	2	Q6FU89	Q6fu89 candida gla
145	87.5	6.3	365	2	Q6KHR7	Q6khr7 mycoplasma	218	85.5	6.1	999	2	Q93JY2	Q93jy2 erwinia chr
146	87.5	6.3	429	2	Q68WP9	Q68wp9 rickettsia	219	85	6.1	304	2	Q96U46	Q96u46 neurospora
147	87.5	6.3	429	2	Q9KRP3	Q9krp3 vibrio chol	220	85	6.1	307	2	Q6F7C6	Q6f7c6 acinetobact
148	87.5	6.3	453	1	TDE2_MOUSE	Q9qzi8 mus musculu	221	85	6.1	333	2	Q6XCC9	Q6xcc9 cyprinus ca
149	87.5	6.3	453	2	Q642W5	Q642w5 clymenella	222	85	6.1	338	1	PSC1_MYCTU	P95303 mycobacteri
150	87.5	6.3	453	2	Q7TNK0	Q7tnk0 rattus norv	223	85	6.1	361	2	Q82VS6	Q82vs6 nitrosomona
151	87.5	6.3	456	2	Q6BQ78	Q6bq78 debaryomyce	224	85	6.1	369	2	Q9N2T7	Q9n2t7 caenorhabdi
152	87.5	6.3	482	1	YFIG_BACSU	P54723 bacillus su	225	85	6.1	419	2	Q8NRU3	Q8nru3 corynebacte
153	87.5	6.3	530	2	Q8EMR7	Q8emr7 oceanobacil	226	85	6.1	427	2	Q7PKH1	Q7pkh1 anopheles g
154	87.5	6.3	544	2	O18061	O18061 caenorhabdi	227	85	6.1	443	2	Q9CEP2	Q9cep2 lactococcus
155	87.5	6.3	547	2	Q824X5	Q824x5 chlamydophi	228	85	6.1	462	2	Q96YE7	Q96ye7 sulfolobus
156	87.5	6.3	671	2	Q73WX6	Q73wx6 mycobacteri	229	85	6.1	497	2	Q6BY36	Q6by36 debaryomyce
157	87.5	6.3	732	2	Q9TJQ2	Q9tjq2 rustia sple	230	85	6.1	498	2	Q9QXP0	Q9qxp0 mus musculu
158	87.5	6.3	1687	2	Q6QI17	Q6qil7 rattus norv	231	85	6.1	522	2	Q9B8X9	Q9b8x9 fasciola he
159	87	6.2	261	2	Q7VLV2	Q7vlv2 haemophilus	232	85	6.1	524	2	Q8U4T9	Q8u4t9 halobacteri
160	87	6.2	271	2	Q6FFL1	Q6ffl1 acinetobact	233	85	6.1	543	2	Q83GL8	Q83gl8 tropheryma
161	87	6.2	396	2	Q8XSA2	Q8xsa2 escherichia	234	85	6.1	543	2	Q83NH2	Q83nh2 tropheryma
162	87	6.2	410	2	Q62BS8	Q62bs8 burkholderi	235	85	6.1	658	2	Q6XJH9	Q6xjh9 sideroxylon
163	87	6.2	410	2	Q63LLO	Q63llo burkholderi	236	85	6.1	658	2	Q6XJ14	Q6xji4 sideroxylon
164	87	6.2	435	1	EXOQ_RHIME	Q02729 rhizobium m	237	85	6.1	845	2	Q80Z08	Q80z08 mus musculu
165	87	6.2	613	2	Q9I4D1	Q9i4d1 pseudomonas	238	85	6.1	1166	1	CYA6_RAT	Q03343 rattus norv
166	87	6.2	928	2	Q9LEC9	Q9lec9 solanum tub	239	84.5	6.1	205	2	Q8BL29	Q8bl29 mus musculu
167	86.5	6.2	301	2	Q970T4	Q970t4 sulfolobus	240	84.5	6.1	269	2	Q837L9	Q837l9 enterococcu
168	86.5	6.2	368	2	Q839R1	Q839r1 enterococcu	241	84.5	6.1	283	2	Q65D18	Q65dl8 bacillus li
169	86.5	6.2	400	1	YCEI_BACSU	Q34691 bacillus su	242	84.5	6.1	323	2	Q7MYX3	Q7myx3 photorhabdu
170	86.5	6.2	440	2	Q9BXT8	Q9bkt8 caenorhabdi	243	84.5	6.1	394	2	Q7Q0F3	Q7q0f3 anopheles g
171	86.5	6.2	547	2	Q6N8M3	Q6n8m3 rhodopsendo	244	84.5	6.1	395	2	Q6ND83	Q6nd83 rhodopsendo
172	86.5	6.2	557	2	Q8ZXC1	Q8zxc1 pyrobaculum	245	84.5	6.1	405	2	Q65FD5	Q65fd5 bacillus li
173	86.5	6.2	583	2	Q8Y9B6	Q8y9b6 listeria mo	246	84.5	6.1	408	2	Q7XB13	Q7xb13 triticum ae
174	86.5	6.2	586	2	Q7ZV33	Q7zv33 brachydanio	247	84.5	6.1	453	1	TDE2_HUMAN	Q9nrx5 homo sapien
175	86.5	6.2	659	2	Q8MGF7	Q8mgf7 nardostachy	248	84.5	6.1	453	2	Q9RNX3	Q9rnrx3 rhizobium e
176	86.5	6.2	732	2	Q9TJV8	Q9tjv8 chimarrhis	249	84.5	6.1	463	2	Q66C42	Q66c42 yersinia ps
177	86.5	6.2	770	2	Q9YCS4	Q9ycs4 aeropyrum p	250	84.5	6.1	463	2	Q8ZFW8	Q8zfw8 yersinia pe

251 84.5 6.1 473 2 Q65N12 Q65n12 bacillus li
252 84.5 6.1 479 2 Q651L0 Q65110 oryza sativ
253 84.5 6.1 479 2 Q9WZ89 Q9wz89 thermotoga
254 84.5 6.1 491 2 Q18154 Q18154 caenorhabdi
255 84.5 6.1 515 2 Q9LN48 Q9ln48 arabadopsis
256 84.5 6.1 562 2 Q9FLI8 Q9fli8 arabadopsis
257 84.5 6.1 589 2 Q95ZY6 Q95zy6 caenorhabdi
258 84.5 6.1 638 2 Q33749 Q33749 arabacia lix
259 84.5 6.1 702 2 Q9TLF1 Q9tlf1 lindenbergi
260 84.5 6.1 820 2 O45585 O45585 caenorhabdi
261 84.5 6.1 913 2 Q7UJI4 Q7uji4 rhodopirell
262 84 6.0 172 2 Q9TA01 Q9ta01 lampetra fl
263 84 6.0 234 2 Q99N04 Q99n04 mus musculu
264 84 6.0 295 2 Q7YFS4 Q7yfs4 neivamyrmex
265 84 6.0 318 2 Q97NY1 Q97ny1 streptococc
266 84 6.0 329 2 Q8U0A2 Q8u0a2 pyrococcus
267 84 6.0 403 2 Q7MUU1 Q7muu1 porphyromon
268 84 6.0 408 2 Q83MR3 Q83mr3 tropheryma
269 84 6.0 408 2 Q83N96 Q83n96 tropheryma
270 84 6.0 460 2 O59186 O59186 pyrococcus
271 84 6.0 478 2 Q74F67 Q74f67 geobacter s
272 84 6.0 492 2 Q7QAI6 Q7qai6 anopheles g
273 84 6.0 575 2 Q9I642 Q9i642 pseudomonas
274 84 6.0 597 2 Q9KUW6 Q9kuw6 vibrio chol
275 84 6.0 736 2 Q9TJS1 Q9tjs1 pauridianth
276 84 6.0 830 2 Q6C772 Q6c772 yarowia li
277 84 6.0 935 2 Q9ZP04 Q9zpz04 tropaeolum
278 84 6.0 4083 1 DYHC ASHGO Q9clm7 ashbya goss
279 83.5 6.0 261 1 YRBE_HAEIN P45030 haemophilus
280 83.5 6.0 295 2 Q9JVJ1 Q9jvj1 neisseria m
281 83.5 6.0 324 2 Q8XX91 Q8xx91 ralstonia s
282 83.5 6.0 330 2 Q8AA46 Q8aa46 bacteroides
283 83.5 6.0 333 2 Q8E4D6 Q8e4d6 streptococc
284 83.5 6.0 468 2 Q8XXY8 Q8xky8 clostridium
285 83.5 6.0 509 2 Q8IA95 Q8ia95 caenorhabdi
286 83.5 6.0 521 1 YJBC SCHPO Q74949 schizosacch
287 83.5 6.0 521 2 Q875S7 Q875s7 saccharomyc
288 83.5 6.0 531 2 Q83EA0 Q83ea0 coxiella bu
289 83.5 6.0 605 2 Q9L1F6 Q9l1f6 streptomyce
290 83.5 6.0 638 1 NUSM_PARLI P12776 paracentrot
291 83.5 6.0 693 2 Q85GD2 Q85gd2 nardostachy
292 83.5 6.0 736 2 Q9TJZ7 Q9tjz7 anthospermu
293 83.5 6.0 743 2 Q8WH76 Q8wh76 forgesia ra
294 83.5 6.0 976 2 Q6FKX5 Q6fkx5 candida gla
295 83.5 6.0 1829 2 Q86HD9 Q86hd9 dictyosteli
296 83 6.0 305 2 Q8YWR6 Q8ywr6 anabaena sp
297 83 6.0 318 2 Q8DNJ4 Q8dnj4 streptococc
298 83 6.0 321 1 O5V1 HUMAN Q9ugf6 homo sapien
299 83 6.0 321 2 Q6NTB5 Q6ntb5 homo sapien
300 83 6.0 427 2 Q7P8Q1 Q7p8q1 rickettsia
301 83 6.0 427 2 Q92HP5 Q92hp5 rickettsia
302 83 6.0 457 2 Q8U1E5 Q8u1e5 pyrococcus
303 83 6.0 460 2 Q9V0Y7 Q9v0y7 pyrococcus
304 83 6.0 466 2 Q7VNG8 Q7vng8 haemophilus
305 83 6.0 467 2 Q6F9F8 Q6f9f8 acinetobact
306 83 6.0 496 2 Q9I4I8 Q9i4i8 pseudomonas
307 83 6.0 587 2 Q87TZ8 Q87tz8 pseudomonas
308 83 6.0 637 1 NUSM_STRPU P15552 strongyloce
309 83 6.0 802 2 Q8SZ78 Q8sz78 drosophila
310 83 6.0 1139 2 Q66DQ6 Q66dq6 yersinia ps
311 83 6.0 1635 2 Q9C1I7 Q9c1i7 mycosphaere
312 83 6.0 2159 2 Q8RUQ1 Q8ruql zea mays (m
313 83 6.0 2159 2 Q8RVL1 Q8rvl1 zea mays (m
314 82.5 5.9 281 2 Q83BV7 Q83bv7 coxiella bu
315 82.5 5.9 346 2 Q8TQ84 Q8tq84 methanosarc
316 82.5 5.9 368 2 Q72KY8 Q72ky8 thermus the
317 82.5 5.9 391 1 EPT1_YEAST P22140 saccharomyc
318 82.5 5.9 400 2 Q7M9I6 Q7m9i6 wolinnella s
319 82.5 5.9 418 2 Q9HXM9 Q9hxm9 pseudomonas
320 82.5 5.9 437 2 Q8IKE3 Q8ike3 plasmodium
321 82.5 5.9 439 2 Q8P5I4 Q8p5i4 xanthomonas
322 82.5 5.9 448 2 Q6DVM4 Q6dvm4 triops long
323 82.5 5.9 451 2 Q82CI8 Q82ci8 streptomyce

324 82.5 5.9 452 2 Q9ZKR4 Q9zkr4 helicobacte
325 82.5 5.9 462 2 Q6F0L1 Q6f0l1 mesoplasma
326 82.5 5.9 471 2 Q88SS9 Q88ss9 lactobacill
327 82.5 5.9 478 2 Q8EEL5 Q8eel5 shewanella
328 82.5 5.9 486 2 Q82YJ7 Q82yj7 enterococcu
329 82.5 5.9 494 1 NU4M_TRIRU Q82yj7 trichophyto
330 82.5 5.9 508 2 Q950R5 Q950r5 spizellomyc
331 82.5 5.9 543 2 Q7Z5I7 Q7z5i7 homo sapien
332 82.5 5.9 548 2 Q6AAJ7 Q6aaaj7 propionibac
333 82.5 5.9 596 1 AGP2_YEAST P38090 saccharomyc
334 82.5 5.9 620 2 Q7S5R8 Q7s5r8 neurospora
335 82.5 5.9 623 2 Q98P35 Q98p35 rhizobium l
336 82.5 5.9 640 2 Q6MB47 Q6mb47 parachlamyd
337 82.5 5.9 671 2 Q751I3 Q75i13 ashbya goss
338 82.5 5.9 680 2 Q8SL84 Q8sl84 nardostachy
339 82.5 5.9 680 2 Q70SP4 Q70sp4 limoseilla m
340 82.5 5.9 704 2 Q9SCD0 Q9scd0 gustavia su
341 82.5 5.9 733 2 Q8VXB8 Q8vxb8 oryza sativ
342 82.5 5.9 1457 2 Q9HCE0 Q9hce0 homo sapien
343 82.5 5.9 2520 2 Q7PPE3 Q7ppe3 anopheles g
344 82 82 219 2 Q75250 Q75250 homo sapien
345 82 82 267 2 Q88HZ2 Q88hz2 pseudomonas
346 82 82 299 1 T2R3_RAT Q9jku0 rattus norv
347 82 82 313 2 Q87GV0 Q87gv0 vibrio para
348 82 82 317 2 Q9K6Y6 Q9k6y6 bacillus ha
349 82 82 327 2 Q9KT03 Q9kt03 vibrio chol
350 82 82 339 2 Q84ET2 Q84et2 uncultured
351 82 82 356 2 Q9FZ96 Q9fz96 arabadopsis
352 82 82 356 2 Q9M7R1 Q9m7r1 arabadopsis
353 82 82 359 2 Q97C50 Q97c50 thermoplasm
354 82 82 389 2 O25590 O25590 helicobacte
355 82 82 405 2 Q983X3 Q983x3 rhizobium l
356 82 82 446 1 CITN_KLEPN P31602 klebsiella
357 82 82 459 2 Q70XF0 Q70xf0 dromiciops
358 82 82 465 2 Q74M77 Q74m77 nanoarchaeu
359 82 82 488 2 Q93YP9 Q93yp9 arabadopsis
360 82 82 494 2 Q6F0R2 Q6f0r2 mesoplasma
361 82 82 497 2 Q97A43 Q97a43 thermoplasm
362 82 82 498 2 Q73GM3 Q73gw3 wolbachia p
363 82 82 545 2 Q8FNV5 Q8fnv5 corynebacte
364 82 82 548 2 Q9A8F3 Q9a8f3 caulobacter
365 82 82 557 1 YCQ4_SCHPO Q74537 schizosacch
366 82 82 557 2 Q8G3S6 Q8g3s6 bifidobacte
367 82 82 573 2 Q09932 Q09932 caenorhabdi
368 82 82 594 2 Q7T709 Q7t709 citrus tris
369 82 82 706 2 O45283 O45283 caenorhabdi
370 82 82 748 2 Q6A6C2 Q6a6c2 propionibac
371 82 82 881 2 Q6F8D1 Q6f8d1 acinetobact
372 82 82 884 2 Q8ER30 Q8er30 oceanobacil
373 82 82 1029 2 Q6KAN9 Q6kan9 mus musculu
374 82 82 1139 2 Q8ZC91 Q8zc91 yersinia pe
375 82 82 1156 2 Q74WP6 Q74wp6 yersinia pe
376 82 82 1168 1 CYA6_HUMAN Q43306 homo sapien
377 81.5 5.9 205 2 Q97PC0 Q97pc0 streptococc
378 81.5 5.9 205 2 Q8CYE9 Q8cye9 streptococc
379 81.5 5.9 268 2 Q7MKQ7 Q7mkq7 vibrio vuln
380 81.5 5.9 268 2 Q8D9M9 Q8d9m9 vibrio vuln
381 81.5 5.9 292 2 Q92DG0 Q92dgo listeria in
382 81.5 5.9 307 1 UPP2_CLOAB Q97kf6 clostridium
383 81.5 5.9 321 2 Q94VH0 Q94vh0 varanus gou
384 81.5 5.9 325 2 Q973Q6 Q973q6 sulfolobus
385 81.5 5.9 351 2 Q9FZ95 Q9fz95 arabadopsis
386 81.5 5.9 399 2 Q8NCC4 Q8ncc4 homo sapien
387 81.5 5.9 425 2 Q88CV8 Q88cv8 pseudomonas
388 81.5 5.9 436 2 Q7YZ03 Q7yz03 cryptospori
389 81.5 5.9 438 2 Q9HUD9 Q9hud9 pseudomonas
390 81.5 5.9 454 2 Q884R2 Q884r2 pseudomonas
391 81.5 5.9 454 2 Q89WU1 Q89wu1 bradyrhizob
392 81.5 5.9 467 2 Q9W1Z2 Q9w1z2 drosophila
393 81.5 5.9 485 2 O18063 O18063 caenorhabdi
394 81.5 5.9 485 2 Q8SYB7 Q8syb7 drosophila
395 81.5 5.9 485 2 Q9W1Z3 Q9w1z3 drosophila
396 81.5 5.9 510 2 Q34523 Q34523 fasciola he

397	81.5	5.9	535	2	Q53111	Q53111 rhodobacter	470	80.5	5.8	536	2	Q6MEN5	Q6men5 parachlamyid
398	81.5	5.9	626	2	Q8XUM7	Q8xum7 ralstonia s	471	80.5	5.8	590	1	CAN1_YEAST	P04817 saccharomyc
399	81.5	5.9	711	2	Q6LH73	Q6lh73 photobacter	472	80.5	5.8	637	2	O21277	Q21277 reclinomona
400	81.5	5.9	713	2	Q9VMG4	Q9vmg4 drosophila	473	80.5	5.8	650	2	Q7PMQ9	Q7pmq9 anopheles g
401	81.5	5.9	724	2	Q8MRA8	Q8mra8 drosophila	474	80.5	5.8	660	2	Q891N8	Q891n8 clostridium
402	81.5	5.9	724	2	Q9TJZ6	Q9tjz6 alseis lugo	475	80.5	5.8	728	2	Q98702	Q98702 luculia gra
403	81.5	5.9	731	2	Q9TJT2	Q9tjt2 hillia trif	476	80.5	5.8	732	2	Q9TJY9	Q9tjy9 calycophyll
404	81.5	5.9	732	2	Q9TJS0	Q9tjs0 pogonopus s	477	80.5	5.8	834	1	NAH3_HUMAN	P48764 homo sapien
405	81.5	5.9	734	2	Q98706	Q98706 chiococca r	478	80	5.7	834	1	NAH3_HUMAN	Q81kj3 bacillus an
406	81.5	5.9	741	2	Q71QV9	Q71qv9 siegesbecki	479	80	5.7	266	2	Q9HXP7	Q9hxp7 pseudomonas
407	81.5	5.9	855	2	Q6BGA9	Q6bga9 paramecium	480	80	5.7	268	2	Q76FP9	Q76fp9 styela plic
408	81.5	5.9	4960	2	Q7PZB3	Q7pzb3 anopheles g	481	80	5.7	277	2	Q818H6	Q818h6 bacillus ce
409	81	5.8	226	2	Q816R9	Q816r9 bacillus ce	482	80	5.7	285	2	Q6YQJ4	Q6yqj4 onion yello
410	81	5.8	293	1	Y417_CHLTR	Q84422 chlamydia t	483	80	5.7	286	2	Q63CM0	Q63cm0 bacillus ce
411	81	5.8	293	2	Q92WD8	Q92wd8 rhizobium m	484	80	5.7	286	2	Q81RV2	Q81rv2 bacillus an
412	81	5.8	313	1	RBN_VIBVU	Q8dds2 vibrio vuln	485	80	5.7	286	2	Q6HK25	Q6hk25 bacillus th
413	81	5.8	313	1	RBN_VIBVY	Q7mg07 vibrio vuln	486	80	5.7	291	2	Q8UIQ9	Q8uiq9 agrobacteri
414	81	5.8	375	2	P95505	P95505 prochloroth	487	80	5.7	299	2	Q6AL50	Q6al50 desulfotale
415	81	5.8	382	2	Q7PO40	Q7pg40 anopheles g	488	80	5.7	322	2	Q9GEH0	Q9geh0 memecylon b
416	81	5.8	382	2	Q918P4	Q918p4 cyprinus ca	489	80	5.7	339	2	Q84ET1	Q84et1 prochloroth
417	81	5.8	396	2	Q83KE0	Q83ke0 shigella fl	490	80	5.7	363	2	Q8KR39	Q8kr39 clostridium
418	81	5.8	422	2	Q6ESP5	Q6esp5 oryza sativ	491	80	5.7	391	2	Q6LY81	Q6ly81 methanococc
419	81	5.8	422	2	Q8Y1K4	Q8y1k4 ralstonia s	492	80	5.7	429	1	ARSB_STAAU	P30329 staphylococ
420	81	5.8	438	2	Q8X4U5	Q8x4u5 escherichia	493	80	5.7	429	2	Q9AC73	Q9ac73 staphylococ
421	81	5.8	461	1	YCUJ_ECOLI	Q76037 escherichia	494	80	5.7	439	2	Q8PGX4	Q8pgx4 xanthomonas
422	81	5.8	479	2	Q87155	Q87155 vibrio chol	495	80	5.7	445	2	Q6NFO1	Q6nf01 corynebacte
423	81	5.8	485	2	Q7PQT4	Q7pqt4 anopheles g	496	80	5.7	451	2	Q6I7X8	Q6i7x8 leptotyphlo
424	81	5.8	487	2	Q9FRL3	Q9frl3 arabidopsis	497	80	5.7	472	2	Q9N5Q8	Q9n5q8 caenorhabdi
425	81	5.8	515	2	Q8TF71	Q8tf71 homo sapien	498	80	5.7	488	2	Q966D7	Q966d7 caenorhabdi
426	81	5.8	544	1	YRT3_CAEEL	Q10046 caenorhabdi	499	80	5.7	516	2	Q94JG1	Q94jg1 oryza sativ
427	81	5.8	548	2	Q8AA29	Q8aa29 bacteroides	500	80	5.7	558	2	Q6XRA4	Q6xra4 uncultured
428	81	5.8	550	2	Q7NZQ0	Q7nzz0 chromobacte	501	80	5.7	657	2	Q6XJW6	Q6xjm6 inhambanell
429	81	5.8	595	2	Q91MJ8	Q91mj8 menangle vi	502	80	5.7	671	2	Q7WXB7	Q7wxb7 alcaligenes
430	81	5.8	608	2	Q7QP79	Q7qp79 giardia lam	503	80	5.7	699	2	Q9TLF3	Q9tlf3 hemiphragma
431	81	5.8	647	2	Q9GEU0	Q9geu0 samolus val	504	80	5.7	702	2	O19823	O19823 alsobia sp.
432	81	5.8	657	2	Q6XJ11	Q6xj11 sideroxylon	505	80	5.7	714	2	Q73Y59	Q73y59 mycobacteri
433	81	5.8	710	2	O19824	Q19824 cobananthus	506	80	5.7	740	2	Q9TJU4	Q9tju4 cephalanthu
434	81	5.8	724	2	Q9GF06	Q9gf06 jacquinia u	507	80	5.7	740	2	Q8ZQN3	Q8zqn3 salmonella
435	81	5.8	734	2	Q9THV8	Q9thv8 rondeletia	508	80	5.7	902	2	Q9K9X9	Q9k9x9 bacillus ha
436	81	5.8	875	2	Q9V8U1	Q9v8ul drosophila	509	80	5.7	1067	2	Q8EJ80	Q8ej80 shewanella
437	81	5.8	971	2	Q68XX4	Q68xx4 rickettsia	510	80	5.7	1123	2	Q9LYR7	Q9lyr7 arabidopsis
438	81	5.8	1102	2	Q88CW3	Q88cw3 pseudomonas	511	80	5.7	1480	2	Q6C5L2	Q6c5l2 yarrowia li
439	81	5.8	2187	1	POLG_CXB2O	Q9ylg5 c genome po	512	79.5	5.7	234	2	Q6JCS9	Q6jcs9 aleuoroplatu
440	80.5	5.8	162	2	Q7NN16	Q7nnl6 gloeobacter	513	79.5	5.7	264	2	Q6ITH2	Q6ith2 cercaria ba
441	80.5	5.8	261	2	Q6L7B2	Q6l7b2 photobacter	514	79.5	5.7	264	2	Q6ITI1	Q6iti1 cercaria ba
442	80.5	5.8	288	2	Q85JA0	Q85ja0 clonorchis	515	79.5	5.7	293	2	Q66D49	Q66d49 yersinia ps
443	80.5	5.8	291	2	Q746X4	Q746x4 geobacter s	516	79.5	5.7	296	2	Q93KC0	Q93kc0 erwinia chr
444	80.5	5.8	316	2	Q647F8	Q647f8 thermoprote	517	79.5	5.7	296	2	Q6D4I7	Q6d4i7 erwinia car
445	80.5	5.8	321	2	Q94VD4	Q94vd4 varanus pan	518	79.5	5.7	297	2	Q7U561	Q7u561 synechococc
446	80.5	5.8	324	2	Q83Z26	Q83zz6 lamprocysti	519	79.5	5.7	298	2	Q8R257	Q8r257 mus musculu
447	80.5	5.8	333	2	Q8IHX6	Q8ihx6 plasmodium	520	79.5	5.7	308	2	Q6CTH9	Q6cth9 kluyveromyc
448	80.5	5.8	334	2	Q8IQJ7	Q8iqj7 drosophila	521	79.5	5.7	308	2	Q6ACY4	Q6acy4 leifsonia x
449	80.5	5.8	334	2	Q6AWL9	Q6awl9 drosophila	522	79.5	5.7	317	2	Q7UKZ3	Q7ukz3 rhodopirell
450	80.5	5.8	359	2	Q99RB8	Q99rb8 staphylococ	523	79.5	5.7	323	2	Q8DUD9	Q8dud9 streptococc
451	80.5	5.8	359	2	Q7A3I4	Q7a3i4 staphylococ	524	79.5	5.7	384	2	Q88ZD3	Q88zd3 lactobacill
452	80.5	5.8	359	2	Q7A3I4	Q7a3i4 staphylococ	525	79.5	5.7	398	2	Q7NVC7	Q7nvc7 chromobacte
453	80.5	5.8	359	2	Q6G6F7	Q6g6f7 staphylococ	526	79.5	5.7	405	2	Q77085	Q77085 caenorhabdi
454	80.5	5.8	366	2	Q8CWZ5	Q8cwz5 streptococc	527	79.5	5.7	443	2	Q95AK6	Q95ak6 dialypetalu
455	80.5	5.8	393	2	Q8CNG2	Q8cng2 staphylococ	528	79.5	5.7	445	2	Q55937	Q55937 synechocyst
456	80.5	5.8	419	2	Q81NE5	Q81ne5 bacillus an	529	79.5	5.7	445	2	Q6HKB2	Q6hkb2 bacillus th
457	80.5	5.8	433	2	Q66FD9	Q66fd9 yersinia ps	530	79.5	5.7	461	2	Q7UCQ4	Q7ucq4 shigella fl
458	80.5	5.8	433	2	Q74XD2	Q74xd2 yersinia pe	531	79.5	5.7	479	2	Q83RL6	Q83rl6 shigella fl
459	80.5	5.8	433	2	Q8Z1Y7	Q8ziy7 yersinia pe	532	79.5	5.7	485	2	Q73Y55	Q73y55 mycobacteri
460	80.5	5.8	438	2	Q87VV4	Q87vv4 pseudomonas	533	79.5	5.7	499	2	Q9UYP1	Q9uyp1 pyrococcus
461	80.5	5.8	446	2	Q951C1	Q951c1 tetrahymena	534	79.5	5.7	505	2	Q93GK1	Q93gk1 bacillus st
462	80.5	5.8	469	2	P93561	P93561 solanum tub	535	79.5	5.7	517	2	Q6MY57	Q6my57 aspergillus
463	80.5	5.8	470	2	Q9CP91	Q9cp91 pasteurella	536	79.5	5.7	522	2	Q7QJ78	Q7qj78 anopheles g
464	80.5	5.8	473	2	Q34718	Q34718 bacillus su	537	79.5	5.7	539	1	FIXN_AGR77	P98055 agrobacteri
465	80.5	5.8	475	2	Q6LR41	Q6lr41 photobacter	538	79.5	5.7	542	2	Q8YB8	Q8ybw8 brucella me
466	80.5	5.8	523	2	Q8AAx1	Q8aaax1 bacteroides	539	79.5	5.7	542	2	Q8FWF3	Q8fwf3 brucella su
467	80.5	5.8	528	2	Q7DDN3	Q7ddn3 neisseria m	540	79.5	5.7	544	2	Q64940	Q64940 avian infec
468	80.5	5.8	528	2	Q9JRD7	Q9jrd7 neisseria m	541	79.5	5.7	570	2	Q8UF62	Q8uf62 agrobacteri
469	80.5	5.8	531	2	Q6KI84	Q6ki84 mycoplasma	542	79.5	5.7	573	2	Q63FV4	Q63fv4 bacillus ce

543	79.5	5.7	573	2	Q81V13	Q81v13 bacillus an	616	79	5.7	738	2	Q9TJS8	Q9tjs8 morinda cit
544	79.5	5.7	593	2	Q6BM61	Q6bm61 debaryomyce	617	79	5.7	746	2	Q9TLB7	Q9tlb7 digitalis p
545	79.5	5.7	598	2	Q7CZ11	Q7cz11 agrobacteri	618	79	5.7	819	2	O31582	O31582 bacillus su
546	79.5	5.7	600	2	Q6LK0	Q6lk0 photobacter	619	79	5.7	1501	2	Q8C1Q9	Q8ciq9 mus musculu
547	79.5	5.7	613	2	Q8CBQ1	Q8cbq1 mus musculu	620	79	5.7	1521	2	Q80ZZ8	Q80zz8 mus musculu
548	79.5	5.7	628	2	Q67ML1	Q67ml1 symbiobacte	621	79	5.7	1521	2	Q8CGS3	Q8cgs3 mus musculu
549	79.5	5.7	632	2	Q9AZ47	Q9az47 enterobacte	622	79	5.7	1521	2	Q8CIP6	Q8cip6 mus musculu
550	79.5	5.7	669	2	Q6USQ3	Q6usq3 valeriana e	623	79	5.7	2198	2	Q18990	Q18990 caenorhabdi
551	79.5	5.7	677	2	Q6CY48	Q6cy48 kluyveromyc	624	78.5	5.6	169	2	Q9HSA7	Q9hsa7 halobacteri
552	79.5	5.7	695	2	Q9TJS9	Q9tjs9 mussaenda a	625	78.5	5.6	241	1	MCBE_ECOLI	P05528 escherichia
553	79.5	5.7	697	2	Q6YSA9	Q6ysa9 oryza sativ	626	78.5	5.6	242	2	Q6LPC6	Q6lpc6 photobacter
554	79.5	5.7	699	2	Q91YL7	Q91yl7 mus musculu	627	78.5	5.6	264	2	Q61TH4	Q6ith4 cercaria ba
555	79.5	5.7	741	2	Q32132	Q32132 chrysanthem	628	78.5	5.6	264	2	Q6ITI2	Q6iti2 cercaria ba
556	79.5	5.7	831	1	NAH3_RAT	P26433 rattus norv	629	78.5	5.6	298	2	Q65V25	Q65v25 mannheimia
557	79.5	5.7	878	2	Q8MKD0	Q8mk10 drosophila	630	78.5	5.6	298	2	Q73T54	Q73t54 mycobacteri
558	79.5	5.7	976	2	Q96VU4	Q96vu4 blumeria gr	631	78.5	5.6	314	2	Q970C7	Q970c7 sulfolobus
559	79	5.7	154	2	Q42211	Q42211 necturus ma	632	78.5	5.6	316	2	Q7EY23	Q7eyz3 oryza sativ
560	79	5.7	172	1	NU6M_PETMA	Q35544 petromyzon	633	78.5	5.6	320	2	Q9BBU4	Q9bbu4 warnecke m
561	79	5.7	183	1	Y507_HAEIN	P44010 haemophilus	634	78.5	5.6	320	2	Q7ZWS9	Q7zws9 xenopus lae
562	79	5.7	192	2	Q6CYK5	Q6cyk5 erwinia car	635	78.5	5.6	321	2	Q9BBV9	Q9bbv9 mouriri hel
563	79	5.7	226	2	Q6HCDO	Q6hcd0 bacillus th	636	78.5	5.6	325	2	Q9MRZ1	Q9mrz1 heterocentr
564	79	5.7	229	2	Q8XIK9	Q8xik9 clostridium	637	78.5	5.6	330	2	Q9VU64	Q9vu64 drosophila
565	79	5.7	289	2	Q946J9	Q946j9 medicago tr	638	78.5	5.6	340	2	Q8G845	Q8g845 bifidobacte
566	79	5.7	293	1	Y543_CHLPN	Q9z809 chlamydia p	639	78.5	5.6	356	2	Q8DTT2	Q8dtt2 streptococc
567	79	5.7	293	2	Q9KDZ5	Q9kdz5 bacillus ha	640	78.5	5.6	366	1	YB96_METJA	Q58596 methanococc
568	79	5.7	300	2	Q6HM61	Q6hm61 bacillus th	641	78.5	5.6	389	2	Q93TD9	Q93td9 pseudomonas
569	79	5.7	307	2	Q9JTQ9	Q9jtg9 neisseria m	642	78.5	5.6	389	2	Q87WD8	Q87wd8 pseudomonas
570	79	5.7	310	2	Q7MJN1	Q7mjn1 vibrio vuln	643	78.5	5.6	393	2	Q639K7	Q639k7 bacillus ce
571	79	5.7	310	2	Q8DAH5	Q8dah5 vibrio vuln	644	78.5	5.6	397	2	Q8KW37	Q8kw37 ruegeria sp
572	79	5.7	354	2	Q97C19	Q97c19 thermoplasm	645	78.5	5.6	405	2	Q9U2M5	Q9u2m5 caenorhabdi
573	79	5.7	369	2	Q8PL40	Q8pl40 xanthomonas	646	78.5	5.6	411	2	Q89ZC7	Q89zc7 bacteroides
574	79	5.7	372	2	Q6G1A8	Q6gia8 staphylococ	647	78.5	5.6	412	2	Q99X84	Q99x84 staphylococ
575	79	5.7	373	2	Q8LBH3	Q8lbh3 arabidopsis	648	78.5	5.6	412	2	Q7A856	Q7a856 staphylococ
576	79	5.7	377	2	Q9LXX8	Q9lxx8 arabidopsis	649	78.5	5.6	443	2	Q8ZLW4	Q8zlw4 salmonella
577	79	5.7	381	2	Q6FDD6	Q6fdd6 acinetobact	650	78.5	5.6	447	2	Q6CYW0	Q6cyw0 erwinia car
578	79	5.7	386	2	Q7NCK9	Q7nck9 gloeobacter	651	78.5	5.6	464	2	Q979J8	Q979j8 thermoplasm
579	79	5.7	389	2	Q64Q89	Q64q89 bacteroides	652	78.5	5.6	470	2	Q6C8J1	Q6c8j1 yarrowia li
580	79	5.7	390	2	Q9X158	Q9x158 thermotoga	653	78.5	5.6	471	2	Q6AB86	Q6ab86 propionibac
581	79	5.7	395	1	HMEB_ARCFU	Q29750 archaeoglob	654	78.5	5.6	482	2	Q83AQ0	Q83aq0 coxiella bu
582	79	5.7	409	2	Q6E830	Q6e830 potnia glad	655	78.5	5.6	483	2	Q85MF7	Q85mf7 cyrestis th
583	79	5.7	410	1	Y588_BUCAI	P57648 buchnera ap	656	78.5	5.6	487	2	Q6UWE7	Q6uwe7 homo sapien
584	79	5.7	414	2	Q66R30	Q66r30 saccharomyc	657	78.5	5.6	490	2	Q9AWL1	Q9awl1 oryza sativ
585	79	5.7	429	2	Q63YG8	Q63yg8 burkholderi	658	78.5	5.6	493	2	Q9V0T0	Q9v0t0 pyrococcus
586	79	5.7	438	2	Q7ACT1	Q7act1 escherichia	659	78.5	5.6	501	2	Q8FB10	Q8fb10 escherichia
587	79	5.7	438	2	Q8FGD5	Q8fgd5 escherichia	660	78.5	5.6	510	2	Q9B8Y2	Q9b8y2 fasciola he
588	79	5.7	443	2	Q6LKM2	Q6lkm2 photobacter	661	78.5	5.6	512	2	Q6ZMD2	Q6zmd2 homo sapien
589	79	5.7	444	2	Q7VT98	Q7vt98 bordetella	662	78.5	5.6	526	2	Q6MUB7	Q6mub7 mycoplasma
590	79	5.7	444	2	Q7W2C1	Q7w2c1 bordetella	663	78.5	5.6	559	2	Q6DCE3	Q6dce3 xenopus lae
591	79	5.7	444	2	Q7WR89	Q7wr89 bordetella	664	78.5	5.6	579	2	O50465	O50465 mycobacteri
592	79	5.7	444	2	Q9KKW1	Q9kkw1 vibrio chol	665	78.5	5.6	583	2	Q950T2	Q950t2 hyaloraphid
593	79	5.7	446	2	Q6L0U0	Q6lou0 picrophilus	666	78.5	5.6	591	2	Q8SXJ9	Q8sxj9 drosophila
594	79	5.7	447	2	Q6GER0	Q6ger0 staphylococ	667	78.5	5.6	591	2	Q9V9U1	Q9v9u1 drosophila
595	79	5.7	453	2	Q8Y8B8	Q8y8b8 listeria mo	668	78.5	5.6	622	1	COX1_BACSU	P24010 bacillus su
596	79	5.7	456	2	Q9HID5	Q9hid5 thermoplasm	669	78.5	5.6	624	2	Q9LYR6	Q9lyr6 arabidopsis
597	79	5.7	456	2	Q7PB27	Q7pb27 rickettsia	670	78.5	5.6	652	2	Q9TIX1	Q9tix1 codon schen
598	79	5.7	464	2	Q8RC72	Q8rc72 thermoanaer	671	78.5	5.6	682	2	Q6USQ0	Q6usq0 valeriana c
599	79	5.7	473	2	O16252	O16252 caenorhabdi	672	78.5	5.6	691	2	Q93YK5	Q93yk5 brassica na
600	79	5.7	481	2	Q62EY5	Q62ey5 burkholderi	673	78.5	5.6	732	2	Q98707	Q98707 mussaenda e
601	79	5.7	489	2	Q97EE9	Q97ee9 clostridium	674	78.5	5.6	732	2	Q9TJP6	Q9tjp6 strumphia m
602	79	5.7	497	2	Q7TNN9	Q7tnn9 rattus norv	675	78.5	5.6	734	2	Q9TJQ0	Q9tjq0 rogiera suf
603	79	5.7	517	2	Q9XYS3	Q9xys3 dictyosteli	676	78.5	5.6	744	2	Q32645	Q32645 menyanthes
604	79	5.7	534	2	Q88Z37	Q88z37 lactobacill	677	78.5	5.6	779	2	Q6A6U5	Q6a6u5 propionibac
605	79	5.7	595	2	Q837Q4	Q837q4 enterococcu	678	78.5	5.6	825	2	Q6N2I5	Q6n2i5 rhodopseudo
606	79	5.7	602	2	Q70XI8	Q70xi8 rhyncholest	679	78.5	5.6	863	2	Q92L62	Q92l62 rhizobium m
607	79	5.7	658	2	Q6XJH8	Q6xjh8 sideroxylon	680	78.5	5.6	1093	2	Q84W30	Q84w30 arabidopsis
608	79	5.7	658	2	Q6XJ12	Q6xji2 sideroxylon	681	78.5	5.6	1289	2	Q7RKA2	Q7rka2 plasmodium
609	79	5.7	658	2	Q6XJL0	Q6xj10 nesoluma po	682	78.5	5.6	1325	2	O64533	O64533 arabidopsis
610	79	5.7	669	1	NU5M_ARATH	P29388 arabidopsis	683	78.5	5.6	2556	2	Q9QH56	Q9qh56 gallid herp
611	79	5.7	682	2	Q69UI4	Q69ui4 oryza sativ	684	78	5.6	158	2	Q9XW23	Q9xw23 caenorhabdi
612	79	5.7	685	2	O19822	O19822 alsobia sp.	685	78	5.6	197	2	Q98CZ0	Q98cz0 rhizobium l
613	79	5.7	688	2	Q8MX1	Q8mx1 sphenoclea	686	78	5.6	227	2	Q8HMJ0	Q8hmj0 carapus ber
614	79	5.7	692	2	Q9TIW2	Q9tiw2 phacelia ca	687	78	5.6	262	2	Q98A38	Q98a38 rhizobium l
615	79	5.7	723	2	O35193	O35193 mus musculu	688	78	5.6	268	2	Q6LZ29	Q6lzz9 methanococc

689	78	5.6	295	2	Q6P8F8	Q6p8f8 xenopus tro	762	77.5	5.6	359	2	Q6GDS8	Q6gds8 staphylococ
690	78	5.6	299	2	Q9QX34	Q9qx34 mus musculu	763	77.5	5.6	363	2	Q9YFU4	Q9yfu4 aeropyrum p
691	78	5.6	307	2	Q9JYR8	Q9jyr8 neisseria m	764	77.5	5.6	367	2	Q67RR1	Q67rr1 symbiobacte
692	78	5.6	327	2	Q974Q0	Q974q0 sulfolobus	765	77.5	5.6	368	2	Q85GB7	Q85gb7 cryptothlad
693	78	5.6	335	1	MRAY CHLMU	Q9plg6 chlamydia m	766	77.5	5.6	399	2	Q978I2	Q978i2 thermoplasm
694	78	5.6	338	2	Q9KY69	Q9ky69 streptomyce	767	77.5	5.6	406	2	Q6DNG7	Q6dng7 glycine max
695	78	5.6	340	2	Q7S3I4	Q7s3i4 neurospora	768	77.5	5.6	436	2	Q6P6X7	Q6p6x7 brachydanio
696	78	5.6	353	2	Q8QOJ7	Q8qoj7 methanosarc	769	77.5	5.6	443	2	Q8TRL4	Q8trl4 methanosarc
697	78	5.6	366	2	Q6SF48	Q65f48 bacillus li	770	77.5	5.6	448	2	Q9XMU9	Q9xmu9 tetrahymena
698	78	5.6	379	2	Q8S169	Q85l69 chimaerohem	771	77.5	5.6	458	2	Q6CZJ3	Q6czj3 erwinia car
699	78	5.6	382	2	Q921S9	Q92l89 rickettsia	772	77.5	5.6	459	2	Q85UJ5	Q85uj5 coturnix ch
700	78	5.6	388	2	Q9RTZ5	Q9rtz5 deinococcus	773	77.5	5.6	460	2	Q7N370	Q7n370 photorhabdu
701	78	5.6	392	2	Q9ESM5	Q9esm5 rattus norv	774	77.5	5.6	461	2	Q8X7F9	Q8x7f9 escherichia
702	78	5.6	396	2	Q8Z581	Q8z581 salmonella	775	77.5	5.6	464	2	Q9I6G9	Q9i6g9 pseudomonas
703	78	5.6	396	2	Q8ZNJ7	Q8znj7 salmonella	776	77.5	5.6	477	2	Q7MKV7	Q7mkv7 vibrio vuln
704	78	5.6	408	2	Q81RH3	Q81rh3 bacillus an	777	77.5	5.6	477	2	Q87PF8	Q87pf8 vibrio para
705	78	5.6	409	1	CIW3 MOUSE	Q35l11 mus musculu	778	77.5	5.6	477	2	Q8D9I1	Q8d9i1 vibrio vuln
706	78	5.6	409	2	Q6HZF9	Q6hzp9 bacillus an	779	77.5	5.6	479	2	Q7AEJ3	Q7aej3 escherichia
707	78	5.6	409	2	Q6HJQ7	Q6hjg7 bacillus th	780	77.5	5.6	492	2	Q7VFT5	Q7vft5 helicobacte
708	78	5.6	411	1	CIW3 RAT	O549i2 rattus norv	781	77.5	5.6	499	2	Q8Z3S3	Q8z3s3 salmonella
709	78	5.6	414	1	YM87 YEAST	Q04835 saccharomyc	782	77.5	5.6	504	2	Q688L6	Q688l6 oryza sativ
710	78	5.6	416	2	Q6VNS3	Q6vns3 mus musculu	783	77.5	5.6	507	2	Q7VQS9	Q7vsg9 bordetella
711	78	5.6	424	2	Q6SPF28	Q6sfz8 uncultured	784	77.5	5.6	507	2	Q7WDH8	Q7wdh8 bordetella
712	78	5.6	428	2	Q6LS34	Q6ls34 photobacter	785	77.5	5.6	510	1	Y382 RICPR	Q9zde9 rickettsia
713	78	5.6	452	2	Q7VAQ3	Q7vaq3 prochloroco	786	77.5	5.6	510	2	Q9LE20	Q9le20 arabidopsi8
714	78	5.6	462	2	Q9Y8L1	Q9y8l1 pyrococcus	787	77.5	5.6	513	2	Q9KLS4	Q9kls4 vibrio chol
715	78	5.6	467	2	Q95JD3	Q95jd3 orectolagus	788	77.5	5.6	520	2	Q32477	Q32477 justicia am
716	78	5.6	474	2	Q8GGM7	Q8ggm7 streptolag	789	77.5	5.6	526	2	O81501	O81501 arabidopsi8
717	78	5.6	486	2	Q8EXR6	Q8ekr6 shewanella	790	77.5	5.6	531	2	Q6YQU3	Q6yqu3 onion yello
718	78	5.6	486	2	Q687I4	Q687i4 mus musculu	791	77.5	5.6	532	1	COX1 RHOCA	P98059 rhodobacter
719	78	5.6	490	2	Q8FP18	Q8fp18 corynebacte	792	77.5	5.6	535	2	Q55577	Q55577 synechocyst
720	78	5.6	495	2	Q6R9L4	Q6r9l4 zea mays (m	793	77.5	5.6	612	2	Q76HH6	Q76hh6 katsuwonus
721	78	5.6	498	2	Q8BVS0	Q8bvs0 mus musculu	794	77.5	5.6	612	2	Q85UE1	Q85ue1 euthynnus a
722	78	5.6	517	2	Q98H22	Q98h22 rhizobium l	795	77.5	5.6	617	2	Q7S080	Q7s080 neurospora
723	78	5.6	538	2	Q9JAE1	Q9jae1 mumps virus	796	77.5	5.6	630	1	S6A4 MACMU	Q9myx0 macaca mula
724	78	5.6	551	2	Q8BWG6	Q8bwg6 m mus muscu	797	77.5	5.6	635	2	Q9ASS7	Q9ass7 arabidopsi8
725	78	5.6	553	2	Q6CQ66	Q6cq66 kluyveromyc	798	77.5	5.6	639	2	Q85L86	Q85l86 pisaster oc
726	78	5.6	554	2	Q6NAP5	Q6nap5 rhodopseudo	799	77.5	5.6	648	2	Q8SLR2	Q8slr2 couroupita
727	78	5.6	565	2	Q9F3S8	Q9f3s8 rhodothermu	800	77.5	5.6	649	2	O28449	O28449 archaeoglob
728	78	5.6	573	2	Q72LX4	Q72lx4 leptospira	801	77.5	5.6	660	2	Q6Y1T3	Q6ylt3 lachnanthes
729	78	5.6	574	2	Q72T06	Q72t06 leptospira	802	77.5	5.6	665	2	Q9GGT9	Q9ggt9 dulichium a
730	78	5.6	574	2	Q8F2F8	Q8f2f8 leptospira	803	77.5	5.6	693	2	Q96MV6	Q96mv6 homo sapien
731	78	5.6	658	2	Q6XJL1	Q6xjl1 neolemonnie	804	77.5	5.6	695	2	Q97A18	Q97a18 thermoplasm
732	78	5.6	694	2	Q95677	Q95677 solanum dul	805	77.5	5.6	698	2	Q6BGZ2	Q6bgz2 debaryomyce
733	78	5.6	701	2	O01843	O01843 caenorhabdi	806	77.5	5.6	699	2	Q7YM04	Q7ym04 metternich
734	78	5.6	830	2	Q8PQ88	Q8pga8 xanthomonas	807	77.5	5.6	706	2	Q6MK05	Q6mk05 bdellovibri
735	78	5.6	834	2	Q8E9A7	Q8e9a7 shewanella	808	77.5	5.6	717	1	PAL2 ARATH	P45724 arabidopsi8
736	77.5	5.6	212	2	Q9KAJ4	Q9kaj4 bacillus ha	809	77.5	5.6	717	2	Q8RWP4	Q8rwp4 arabidopsi8
737	77.5	5.6	243	2	Q93RC4	Q93rc4 escherichia	810	77.5	5.6	744	2	Q8N261	Q8n261 homo sapien
738	77.5	5.6	260	2	Q7VV38	Q7vv38 bordetella	811	77.5	5.6	750	2	Q93S90	Q93s90 xanthomonas
739	77.5	5.6	260	2	Q7W0U7	Q7w0u7 bordetella	812	77.5	5.6	839	2	Q8TQ74	Q8tcq74 methanosarc
740	77.5	5.6	260	2	Q7WN67	Q7wn67 bordetella	813	77.5	5.6	855	2	Q75AV9	Q75av9 ashbya goss
741	77.5	5.6	268	2	Q8U2B7	Q8u2b7 pyrococcus	814	77.5	5.6	861	2	Q89FW4	Q89fw4 bradyrhizob
742	77.5	5.6	283	2	Q92WH1	Q92wh1 rhizobium m	815	77.5	5.6	870	2	Q8N639	Q8n639 homo sapien
743	77.5	5.6	287	2	Q6NJG1	Q6njg1 corynebacte	816	77.5	5.6	870	2	Q7Z3F1	Q7z3f1 homo sapien
744	77.5	5.6	288	2	Q9MF61	Q9mf61 beta vulgar	817	77.5	5.6	945	2	Q6FG02	Q6fg02 acinetobact
745	77.5	5.6	288	2	Q9M4S9	Q9m4s9 allium cepa	818	77.5	5.6	953	1	CW43 YEAST	P25618 saccharomyc
746	77.5	5.6	291	2	Q6ASD9	Q6asd9 desulfotale	819	77.5	5.6	1118	2	Q9HUE7	Q9hue7 pseudomonas
747	77.5	5.6	292	2	Q8Y8N6	Q8y8n6 listeria mo	820	77.5	5.6	1402	1	Y232 HUMAN	Q92628 homo sapien
748	77.5	5.6	292	2	Q721V7	Q721v7 listeria mo	821	77	5.5	181	2	Q8ZU94	Q8zu94 pyrobaculum
749	77.5	5.6	293	2	Q8ZGV5	Q8zgv5 yersinia pe	822	77	5.5	262	2	Q8KJ17	Q8kji7 rhizobium l
750	77.5	5.6	293	2	Q88E98	Q88e98 pseudomonas	823	77	5.5	269	2	Q73K03	Q73k03 treponema d
751	77.5	5.6	296	2	Q92ZH0	Q92zh0 rhizobium m	824	77	5.5	277	2	Q730Q6	Q730q6 bacillus ce
752	77.5	5.6	308	2	Q660J1	Q660j1 borrelia ga	825	77	5.5	282	2	Q8Y7M2	Q8y7m2 listeria mo
753	77.5	5.6	312	2	Q8VG20	Q8vg20 mus musculu	826	77	5.5	282	2	Q720H2	Q720h2 listeria mo
754	77.5	5.6	312	2	Q7TR57	Q7tr57 mus musculu	827	77	5.5	284	2	O21311	O21311 tetrahymena
755	77.5	5.6	313	2	Q7TS53	Q7ts53 mus musculu	828	77	5.5	284	2	Q9T7M5	Q9t7m5 tetrahymena
756	77.5	5.6	317	2	Q8RFJ5	Q8rfj5 fusobacteri	829	77	5.5	286	2	Q739X4	Q739x4 bacillus ce
757	77.5	5.6	318	1	NULM VARRU	Q94vc3 varanus rud	830	77	5.5	293	2	Q82S88	Q82s88 nitrosomona
758	77.5	5.6	321	2	Q94Vi2	Q94vi2 varanus gig	831	77	5.5	295	2	Q7YFS2	Q7yfs2 neivamyrmex
759	77.5	5.6	327	2	Q9MRZ6	Q9mrz6 comolia cor	832	77	5.5	295	2	Q7YFS6	Q7yfs6 nomamyrmex
760	77.5	5.6	335	2	Q9X0N3	Q9x0n3 thermotoga	833	77	5.5	300	2	Q63EN6	Q63en6 bacillus ce
761	77.5	5.6	347	2	Q70RW1	Q70rw1 berardius b	834	77	5.5	302	2	Q81TX5	Q81tx5 bacillus an

835	77	5.5	310	2	Q89YL4	Q89yl4 bacteroides
836	77	5.5	314	2	Q7TRY1	Q7try1 mus musculus
837	77	5.5	321	2	Q94VE3	Q94ve3 varanus mer
838	77	5.5	332	2	Q92UP3	Q92up3 rhizobium m
839	77	5.5	352	2	Q89SN1	Q89sn1 bradyrhizob
840	77	5.5	352	2	Q9W6K3	Q9w6k3 anolis caro
841	77	5.5	353	2	Q9TE65	Q9te65 thalassione
842	77	5.5	354	2	Q6F2N6	Q6f2n6 oryza sativ
843	77	5.5	355	2	Q88DH5	Q88dh5 pseudomonas
844	77	5.5	361	2	Q86JW2	Q86jw2 dictyosteli
845	77	5.5	372	2	Q6DA40	Q6da40 erwinia car
846	77	5.5	387	2	Q89II6	Q89ii6 bradyrhizob
847	77	5.5	390	2	Q7N821	Q7n821 photorhabdu
848	77	5.5	403	2	Q9HIJ3	Q9hij3 thermoplasm
849	77	5.5	417	2	Q97YX9	Q97yx9 sulfolobus
850	77	5.5	438	1	SHIA_ECOLI	P76350 escherichia
851	77	5.5	438	2	Q34739	O34739 bacillus su
852	77	5.5	451	2	Q73GR0	Q73gr0 wolbachia p
853	77	5.5	459	2	Q8SFC7	Q8sfc7 arenaria in
854	77	5.5	460	2	Q87GT8	Q87gt8 vibrio para
855	77	5.5	461	2	Q73JZ7	Q73jz7 treponema d
856	77	5.5	471	2	Q97U43	Q97u43 sulfolobus
857	77	5.5	476	2	Q7T3R8	Q7t3r8 fugu rubrip
858	77	5.5	478	2	Q91WN3	Q91wn3 mus musculu
859	77	5.5	485	2	Q87J14	Q87j14 vibrio para
860	77	5.5	486	2	Q6FLH2	Q6flh2 candida gla
861	77	5.5	486	2	Q6G4T8	Q6g4t8 bartonella
862	77	5.5	506	2	Q80XM3	Q80xm3 mus musculu
863	77	5.5	519	1	SC59_YEAST	P20048 saccharomyc
864	77	5.5	532	2	Q88CD0	Q88cd0 pseudomonas
865	77	5.5	536	2	Q88KJ9	Q88kj9 rhizobium l
866	77	5.5	540	2	Q82SN0	Q82sn0 nitrosomona
867	77	5.5	551	1	FIXN_AZOCA	P98056 azorhizobiu
868	77	5.5	551	2	Q73V35	Q73v35 mycobacteri
869	77	5.5	552	2	Q81B60	Q81b60 bacillus ce
870	77	5.5	579	2	Q8YSW1	Q8ysw1 anabaena sp
871	77	5.5	580	2	Q7PVG5	Q7pvg5 anopheles g
872	77	5.5	588	2	Q6ALD0	Q6ald0 desulfotale
873	77	5.5	597	2	Q6CLT4	Q6clt4 kluyveromyc
874	77	5.5	625	2	Q65DA4	Q65da4 bacillus li
875	77	5.5	662	1	CYOB_BUCAI	P57543 buchnera ap
876	77	5.5	672	2	Q6G0V1	Q6g0v1 bartonella
877	77	5.5	679	2	Q6H9F9	Q6h9f9 lancea tibe
878	77	5.5	695	2	Q7YM01	Q7ym01 vestia lyci
879	77	5.5	710	2	Q19239	Q19239 caenorhabdi
880	77	5.5	716	2	Q8VXB0	Q8vxb0 oryza sativ
881	77	5.5	725	2	Q9TJP9	Q9tjp9 spermacoce
882	77	5.5	731	2	Q8MA29	Q8ma29 cyclocheilo
883	77	5.5	739	2	Q32109	Q32109 conyza sp.
884	77	5.5	749	2	Q83812	Q83812 treponema p
885	77	5.5	778	2	Q652J4	Q652j4 oryza sativ
886	77	5.5	785	1	POT5_ARATH	Q9m7k4 arabidopsis
887	77	5.5	808	2	Q35190	O35190 mus musculu
888	77	5.5	907	2	Q9ZP26	Q9zp26 arabidopsis
889	77	5.5	915	2	Q9S7Y7	Q9s7y7 arabidopsis
890	77	5.5	1138	2	Q96YE8	Q96ye8 sulfolobus
891	77	5.5	1176	2	Q6F749	Q6f749 acinetobact
892	77	5.5	1240	2	Q8DKE8	Q8dke8 synechococc
893	77	5.5	4706	2	Q9FN44	Q9fn44 arabidopsis
894	77	5.5	152	2	Q9YDP6	Q9ydp6 aeropyrum p
895	76.5	5.5	175	2	Q8IJT0	Q8ijt0 plasmodium
896	76.5	5.5	243	2	Q8ZU92	Q8zu92 pyrobaculum
897	76.5	5.5	259	2	Q90572	Q90572 ginglymosto
898	76.5	5.5	262	1	CTE2_HUMAN	Q8n6m3 homo sapien
899	76.5	5.5	269	2	P96581	P96581 bacillus su
900	76.5	5.5	284	1	FOCA_HAEIN	P43756 haemophilus
901	76.5	5.5	289	2	Q22541	Q22541 oryza sativ
902	76.5	5.5	300	1	YIIP_ECOLI	P32159 escherichia
903	76.5	5.5	301	2	Q23340	Q23340 caenorhabdi
904	76.5	5.5	301	2	Q9KSV5	Q9ksv5 vibrio chol
905	76.5	5.5	305	2	Q9KFT1	Q9kft1 bacillus ha
906	76.5	5.5	311	1	PAQ3_MOUSE	Q6tcg8 mus musculu
907	76.5	5.5	311	2	Q6AXP7	Q6axp7 rattus norv

908	76.5	5.5	312	2	Q6PC57	Q6pc57
909	76.5	5.5	316	2	Q7JLH4	Q7jlh4 caenorhabdi
910	76.5	5.5	319	2	Q6Q7V6	Q6q7v6 eriocnema f
911	76.5	5.5	319	2	Q9YH55	Q9yh55 gallus gall
912	76.5	5.5	321	2	Q94VD1	Q94vdi varanus pan
913	76.5	5.5	321	2	Q9GEG8	Q9geg8 mouriri gui
914	76.5	5.5	326	2	Q9GEH7	Q9geh7 heterocentr
915	76.5	5.5	327	2	Q8DLE0	Q8dle0 synechococc
916	76.5	5.5	333	2	Q9MRX5	Q9mrx5 tibouchina
917	76.5	5.5	334	2	Q9V056	Q9v056 pyrococcus
918	76.5	5.5	339	2	Q7U8B3	Q7u8b3 synechococc
919	76.5	5.5	339	2	Q7VCR6	Q7vcr6 prochloroco
920	76.5	5.5	344	1	TA10_RAT	Q923y0 rattus norv
921	76.5	5.5	353	2	Q9TE67	Q9te67 rhizosoleni
922	76.5	5.5	361	2	Q8AY37	Q8ay37 gallus gall
923	76.5	5.5	369	2	Q8G6D1	Q8g6d1 bifidobacte
924	76.5	5.5	370	2	Q8YHY9	Q8yhy9 brucella me
925	76.5	5.5	370	2	Q8FZX1	Q8fzx1 brucella su
926	76.5	5.5	382	2	Q85187	Q85187 vibrio chol
927	76.5	5.5	385	2	Q8IZ31	Q8iz31 homo sapien
928	76.5	5.5	388	2	Q9N4S1	Q9n4s1 caenorhabdi
929	76.5	5.5	395	2	Q8Z700	Q8z700 salmonella
930	76.5	5.5	395	2	Q8ZPI5	Q8zpi5 salmonella
931	76.5	5.5	396	2	Q9XDR1	Q9xdr1 actinobacil
932	76.5	5.5	399	2	Q74HG7	Q74bg7 lactobacill
933	76.5	5.5	404	2	Q81E11	Q81e11 bacillus ce
934	76.5	5.5	419	2	Q638Y3	Q638y3 bacillus ce
935	76.5	5.5	424	2	Q74M02	Q74m02 lactobacill
936	76.5	5.5	431	2	Q9K7K1	Q9k7k1 bacillus ha
937	76.5	5.5	443	2	Q71XS7	Q71xs7 listeria mo
938	76.5	5.5	450	2	Q7QMI8	Q7qmi8 anopheles g
939	76.5	5.5	466	2	Q74HI0	Q74hi0 lactobacill
940	76.5	5.5	474	1	PNTB_HAEIN	P43010 haemophilus
941	76.5	5.5	475	1	HUTM_BACSU	P42087 bacillus su
942	76.5	5.5	480	2	Q8ERF0	Q8erf0 oceanobacil
943	76.5	5.5	486	2	Q8MPU6	Q8mpu6 caenorhabdi
944	76.5	5.5	495	2	Q66E75	Q66e75 yersinia ps
945	76.5	5.5	495	2	Q8ZBT3	Q8zbt3 yersinia pe
946	76.5	5.5	497	2	Q9HL81	Q9hl81 thermoplasm
947	76.5	5.5	498	2	Q8P1I0	Q8p1i0 streptococc
948	76.5	5.5	498	2	Q9A0F5	Q9a0f5 streptococc
949	76.5	5.5	498	2	Q8K803	Q8k803 streptococc
950	76.5	5.5	515	2	Q645E7	Q645e7 oedipina po
951	76.5	5.5	518	2	Q6CLG6	Q6clg6 kluyveromyc
952	76.5	5.5	541	1	AAP2_NEUCR	O59942 neurospora
953	76.5	5.5	548	2	Q9YBH5	Q9ybh5 aeropyrum p
954	76.5	5.5	568	2	Q6PML9	Q6pml9 homo sapien
955	76.5	5.5	568	2	Q9Y6R2	Q9y6r2 homo sapien
956	76.5	5.5	568	2	Q8VYR9	Q8vyr9 arabidopsis
957	76.5	5.5	583	2	Q722T4	Q722t4 listeria mo
958	76.5	5.5	607	2	Q71N57	Q71n57 androsace s
959	76.5	5.5	626	2	Q94243	Q94243 caenorhabdi
960	76.5	5.5	626	2	Q8CMP0	Q8cmp0 staphylococ
961	76.5	5.5	630	1	S6A4_CAVPO	O35899 cavia porce
962	76.5	5.5	631	2	Q8HUU2	Q8huu2 bessera tui
963	76.5	5.5	640	2	Q9GEU2	Q9geu2 primula sik
964	76.5	5.5	661	2	Q9LBY2	Q9lby2 shewanella
965	76.5	5.5	666	2	Q52732	Q52732 rhizobium e
966	76.5	5.5	669	2	Q8HUS3	Q8hus3 milla biflo
967	76.5	5.5	672	2	Q8HUU3	Q8huu3 bessera ele
968	76.5	5.5	673	2	Q8HUT0	Q8hut0 dandya thad
969	76.5	5.5	675	2	Q8HUS1	Q8hus1 muilla cleve
970	76.5	5.5	677	2	Q6R3K6	Q6r3k6 arabidopsis
971	76.5	5.5	683	2	Q34302	O34302 rhizobium e
972	76.5	5.5	696	2	Q9TIV2	Q9tiv2 pholistoma
973	76.5	5.5	705	2	Q9GHQ1	Q9ghq1 pseudonemac
974	76.5	5.5	716	2	Q6N428	Q6n428 rhodopseudo
975	76.5	5.5	724	2	Q6FE05	Q6fe05 acinetobact
976	76.5	5.5	725	1	YGL4_YEAST	P53134 saccharomyc
977	76.5	5.5	727	2	Q8HTN8	Q8htn8 cocculus ca
978	76.5	5.5	729	2	Q96ND6	Q96nd6 homo sapien
979	76.5	5.5	734	2	Q9TJT3	Q9tjt3 guettarda u
980	76.5	5.5	745	2	Q8WH81	Q8wh81 escallonia

Q6pc57	brachydanio
Q7jlh4	caenorhabdi
Q6q7v6	eriocnema f
Q9yh55	gallus gall
Q94vdi	varanus pan
Q9geg8	mouriri gui
Q9geh7	heterocentr
Q8dle0	synechococc
Q9mrx5	tibouchina
Q9v056	pyrococcus
Q7u8b3	synechococc
Q7vcr6	prochloroco
Q923y0	rattus norv
Q9te67	rhizosoleni
Q8ay37	gallus gall
Q8g6d1	bifidobacte
Q8yhy9	brucella me
Q8fzx1	brucella su
Q85187	vibrio chol
Q8iz31	homo sapien
Q9n4s1	caenorhabdi
Q8z700	salmonella
Q8zpi5	salmonella
Q9xdr1	actinobacil
Q74bg7	lactobacill
Q81e11	bacillus ce
Q638y3	bacillus ce
Q74m02	lactobacill
Q9k7k1	bacillus ha
Q71xs7	listeria mo
Q7qmi8	anopheles g
Q74hi0	lactobacill
P43010	haemophilus
P42087	bacillus su
Q8erf0	oceanobacil
Q8mpu6	caenorhabdi
Q66e75	yersinia ps
Q8zbt3	yersinia pe
Q9hl81	thermoplasm
Q8p1i0	streptococc
Q9a0f5	streptococc
Q8k803	streptococc
Q645e7	oedipina po
Q6clg6	kluyveromyc
O59942	neurospora
Q9ybh5	aeropyrum p
Q6pml9	homo sapien
Q9y6r2	homo sapien
Q8vyr9	arabidopsis
Q722t4	listeria mo
Q71n57	androsace s
Q94243	caenorhabdi
Q8cmp0	staphylococ
O35899	cavia porce
Q8huu2	bessera tui
Q9geu2	primula sik
Q9lby2	shewanella
Q52732	rhizobium e
Q8hus3	milla biflo
Q8huu3	bessera ele
Q8hut0	dandya thad
Q8hus1	muilla cleve
Q6r3k6	arabidopsis
O34302	rhizobium e
Q9tiv2	pholistoma
Q9ghq1	pseudonemac
Q6n428	rhodopseudo
Q6fe05	acinetobact
P53134	saccharomyc
Q8htn8	cocculus ca
Q96nd6	homo sapien
Q9tjt3	guettarda u
Q8wh81	escallonia

981	76.5	5.5	745	2	Q8WH88	Q8wh88	escallonia	1054	76	5.5	492	2	Q6FEH2	Q6feh2	acinetobact
982	76.5	5.5	745	2	Q8WH91	Q8wh91	escallonia	1055	76	5.5	494	2	Q6FCQ9	Q6fcq9	acinetobact
983	76.5	5.5	745	2	Q9MTH0	Q9mth0	escallonia	1056	76	5.5	495	2	Q8HCP7	Q8hcp7	oryza sativ
984	76.5	5.5	746	2	Q33117	Q33117	schlechtend	1057	76	5.5	495	2	Q6D831	Q6d831	erwinia car
985	76.5	5.5	803	2	Q9N978	Q9n978	leishmania	1058	76	5.5	497	2	Q7U380	Q7u380	bordetella
986	76.5	5.5	811	2	Q84MS3	Q84ms3	oryza sativ	1059	76	5.5	502	1	ACH7_CHICK	P22770	gallus gall
987	76.5	5.5	823	2	Q649F7	Q649f7	uncultured	1060	76	5.5	502	1	NU2C_MESVI	Q9muq6	mesostigma
988	76.5	5.5	855	2	Q9L2T7	Q9lzt7	arabidopsis	1061	76	5.5	509	2	Q643C9	Q643c9	streptomyce
989	76.5	5.5	1342	1	F7SK_ECO57	Q8x5h9	escherichia	1062	76	5.5	514	2	Q9CPB6	Q9cpb6	pasteurella
990	76.5	5.5	2967	2	O41892	O41892	hepatitis g	1063	76	5.5	518	2	Q6FLP3	Q6flp3	candida gla
991	76	5.5	210	2	Q701X2	Q701x2	uncultured	1064	76	5.5	520	2	Q82WY7	Q82wy7	nitrosomona
992	76	5.5	226	2	Q632U0	Q632u0	bacillus ce	1065	76	5.5	536	2	Q989I2	Q989i2	rhizobium l
993	76	5.5	261	1	ZNUB_HAEIN	P44691	haemophilus	1066	76	5.5	551	2	Q76M72	Q76m72	mus musculu
994	76	5.5	275	2	Q97K81	Q97k81	clostridium	1067	76	5.5	554	2	Q89DA3	Q89da3	bradyrhizob
995	76	5.5	275	2	Q891M8	Q891m8	clostridium	1068	76	5.5	558	1	CX1B_PARDE	P98002	paracoccus
996	76	5.5	277	2	Q634Q7	Q634q7	bacillus ce	1069	76	5.5	570	1	T7S3_HUMAN	Q9ns93	homo sapien
997	76	5.5	277	2	Q81LV5	Q81lv5	bacillus an	1070	76	5.5	573	2	Q6HNC4	Q6hnc4	bacillus th
998	76	5.5	277	2	Q6HDN7	Q6hdn7	bacillus th	1071	76	5.5	574	2	Q8DGC1	Q8dgc1	synechococc
999	76	5.5	281	2	Q92CF3	Q92cf3	listeria in	1072	76	5.5	578	2	Q33024	Q33024	ruellia cil
1000	76	5.5	282	2	Q92I80	Q92i80	rickettsia	1073	76	5.5	580	2	Q85JB7	Q85jb7	harpochytri
1001	76	5.5	282	2	Q9CK77	Q9ck77	pasteurella	1074	76	5.5	612	2	Q94T23	Q94t23	percopsis t
1002	76	5.5	286	2	Q81EN8	Q81en8	bacillus ce	1075	76	5.5	617	2	O45325	O45325	caenorhabdi
1003	76	5.5	287	2	O49874	O49874	lupinus alb	1076	76	5.5	622	2	Q9HEL3	Q9hel3	neurospora
1004	76	5.5	295	2	Q7YFS9	Q7yfs9	labidus coe	1077	76	5.5	644	2	Q7S7W3	Q7s7w3	neurospora
1005	76	5.5	299	2	Q87JX9	Q87jx9	vibrio para	1078	76	5.5	648	2	Q9GEW8	Q9gew8	manilkara z
1006	76	5.5	312	2	Q91ZC1	Q91zcl	mus musculu	1079	76	5.5	656	2	Q639D7	Q639d7	bacillus ce
1007	76	5.5	316	2	Q8QRU3	Q8qru3	pongine her	1080	76	5.5	658	2	Q6XJM3	Q6xjm3	lecomtedoxa
1008	76	5.5	318	2	Q8CN93	Q8cn93	staphylococ	1081	76	5.5	659	2	Q6CAT5	Q6cat5	yarrowia li
1009	76	5.5	321	2	Q6SL25	Q6sl25	argulus ame	1082	76	5.5	659	2	Q8XBE6	Q8xbe6	escherichia
1010	76	5.5	325	2	Q8IQX1	Q8iqx1	drosophila	1083	76	5.5	663	2	Q6CW54	Q6cw54	kluyveromyc
1011	76	5.5	328	2	Q9GEH9	Q9geh9	dichaetanth	1084	76	5.5	686	2	Q80WJ2	Q80wj2	mus musculu
1012	76	5.5	336	2	Q21716	Q21716	caenorhabdi	1085	76	5.5	695	2	Q32508	Q32508	lycium cest
1013	76	5.5	347	2	Q9VWK6	Q9vwk6	drosophila	1086	76	5.5	699	2	Q9SCG5	Q9secg5	claviija int
1014	76	5.5	353	2	Q9TE69	Q9te69	fragilaria	1087	76	5.5	708	2	Q9THW7	Q9thw7	mitrasacme
1015	76	5.5	356	2	Q8D717	Q8d717	vibrio vuln	1088	76	5.5	719	2	Q6EMC0	Q6emc0	lycopersico
1016	76	5.5	361	2	Q7NEP26	Q7npz6	chromobacte	1089	76	5.5	724	2	Q7YX45	Q7yx45	caenorhabdi
1017	76	5.5	365	2	Q9KS99	Q9ks99	vibrio chol	1090	76	5.5	738	2	Q8C0P3	Q8c0p3	mus musculu
1018	76	5.5	371	1	YB2X_HAEIN	O86233	haemophilus	1091	76	5.5	743	2	Q9N2R1	Q9n2r1	drosophila
1019	76	5.5	373	2	Q6FDT2	Q6fdt2	acinetobact	1092	76	5.5	774	2	Q80WJ3	Q80wj3	mus musculu
1020	76	5.5	381	2	Q715Y5	Q715y5	baiomys tay	1093	76	5.5	852	2	O35192	O35192	mus musculu
1021	76	5.5	384	2	Q6FS89	Q6fs89	candida gla	1094	76	5.5	869	2	Q7Q103	Q7q103	anopheles g
1022	76	5.5	400	2	Q812J4	Q812j4	bacillus ce	1095	76	5.5	904	1	COPP_RAT	O35142	rattus norv
1023	76	5.5	400	2	Q83NP3	Q83np3	tropheryma	1096	76	5.5	956	2	Q18129	Q18129	caenorhabdi
1024	76	5.5	411	2	Q9XNZ5	Q9xnz5	chelonus sp	1097	76	5.5	958	2	Q82FM4	Q8zfm4	yersinia pe
1025	76	5.5	415	2	Q88A33	Q88a33	pseudomonas	1098	76	5.5	966	2	Q7PAP6	Q7pap6	rickettsia
1026	76	5.5	415	2	Q915T3	Q915t3	pseudomonas	1099	76	5.5	966	2	Q92JPC3	Q92jc3	rickettsia
1027	76	5.5	418	2	Q6BYU7	Q6byu7	debaryomyce	1100	76	5.5	971	2	Q9ZE42	Q9ze42	rickettsia
1028	76	5.5	422	1	NAH2_METJA	Q58916	methanococc	1101	76	5.5	1052	1	YLD4_SCHPO	O42656	schizosacch
1029	76	5.5	424	2	Q81F43	Q81f43	bacillus ce	1102	76	5.5	1074	1	EMBC_MYCSM	O50393	mycobacteri
1030	76	5.5	429	2	Q6GIZ4	Q6giz4	staphylococ	1103	76	5.5	1165	1	CYA6_MOUSE	O01341	mus musculu
1031	76	5.5	430	2	Q6Y0P0	Q6y0p0	staphylococ	1104	76	5.5	1241	2	Q9U144	Q9ul44	leishmania
1032	76	5.5	430	2	Q6Y0P3	Q6y0p3	staphylococ	1105	76	5.5	1366	2	Q80WJ6	Q80wj6	mus musculu
1033	76	5.5	430	2	Q62B98	Q62b98	burkholderi	1106	76	5.5	1906	2	Q6WGM8	Q6wgm8	lolium mult
1034	76	5.5	430	2	Q63NH2	Q63nh2	burkholderi	1107	76	5.5	3084	2	Q7RSL8	Q7rsl8	plasmodium
1035	76	5.5	431	2	Q61WG4	Q61wg4	lactobacill	1108	75.5	5.4	210	2	O64625	O64625	arabidopsis
1036	76	5.5	432	2	Q6L9W3	Q6l9w3	eucalanus b	1109	75.5	5.4	210	2	Q7VH88	Q7vh88	helicobacte
1037	76	5.5	433	2	Q92M74	Q92m74	rhizobium m	1110	75.5	5.4	233	2	Q8ZJZ0	Q8zjz0	salmonella
1038	76	5.5	443	2	Q76MW1	Q76m71	mus musculu	1111	75.5	5.4	237	2	Q8X803	Q8x803	escherichia
1039	76	5.5	444	1	OPSP_PETMA	O42490	petromyzon	1112	75.5	5.4	240	2	Q9ZM55	Q9zm55	helicobacte
1040	76	5.5	447	2	Q9HPQ2	Q9hpg2	halobacteri	1113	75.5	5.4	252	2	Q31370	Q31370	brachydanio
1041	76	5.5	452	1	TYR1_YEAST	P20049	saccharomyc	1114	75.5	5.4	252	2	Q6SHH1	Q6shh1	uncultured
1042	76	5.5	452	2	Q6SFF4	Q6sff4	uncultured	1115	75.5	5.4	267	2	Q72CM0	Q72cm0	desulfovibr
1043	76	5.5	453	2	Q72IH6	Q72lh6	listeria mo	1116	75.5	5.4	275	2	Q648G2	Q648g2	uncultured
1044	76	5.5	457	2	Q7VUM3	Q7vum3	bordetella	1117	75.5	5.4	295	2	Q7YFS8	Q7yfs8	labidus spi
1045	76	5.5	457	2	Q7W1Z2	Q7wlz2	bordetella	1118	75.5	5.4	295	2	Q93IB9	Q93ib9	staphylococ
1046	76	5.5	457	2	Q7WQX0	Q7wgx0	bordetella	1119	75.5	5.4	295	2	O53619	O53619	staphylococ
1047	76	5.5	459	2	Q8W9B5	Q8w9b5	vombatus ur	1120	75.5	5.4	296	2	Q9HV25	Q9hv25	pseudomonas
1048	76	5.5	460	2	Q8HM18	Q8hm18	caulophryne	1121	75.5	5.4	297	2	Q66E61	Q66e61	yersinia ps
1049	76	5.5	461	2	Q7QJ38	Q7qj38	anopheles g	1122	75.5	5.4	297	2	Q8ZBU5	Q8zbu5	yersinia pe
1050	76	5.5	467	2	Q6WRY0	Q6wry0	xenopus tro	1123	75.5	5.4	298	2	Q8KPE7	Q8kpe7	bartonella
1051	76	5.5	470	2	Q8FAH1	Q8fah1	escherichia	1124	75.5	5.4	300	2	Q7UB82	Q7ub82	shigella fl
1052	76	5.5	479	2	Q87134	Q87134	vibrio chol	1125	75.5	5.4	300	2	Q8ERA7	Q8era7	oceanobacil
1053	76	5.5	480	2	Q912N9	Q912n9	pseudomonas	1126	75.5	5.4	305	2	Q6N132	Q6n132	rhodopseudo

1127	75.5	5.4	306	2	Q83PD6	Q83pd6 shigella fl
1128	75.5	5.4	308	2	Q82N48	Q82n48 streptomyce
1129	75.5	5.4	312	2	Q6QW75	Q6qw75 azospirillu
1130	75.5	5.4	312	2	Q9L449	Q9l449 azospirillu
1131	75.5	5.4	314	2	Q8FBD1	Q8fbd1 escherichia
1132	75.5	5.4	321	2	Q6FYW5	Q6fyw5 bartonella
1133	75.5	5.4	322	2	Q8UCK8	Q8uck8 agrobacteri
1134	75.5	5.4	323	2	Q6GQ05	Q6gq05 xenopus lae
1135	75.5	5.4	324	2	Q9GEH5	Q9geh5 monochaetum
1136	75.5	5.4	338	2	Q9KDX8	Q9kdx8 bacillus ha
1137	75.5	5.4	343	2	Q6FUK1	Q6fuk1 candida gla
1138	75.5	5.4	352	2	Q7IS48	Q7ls48 ophiopholis
1139	75.5	5.4	353	2	Q99380	Q99380 chorda filu
1140	75.5	5.4	359	2	Q7VGZ9	Q7vgz9 helicobacte
1141	75.5	5.4	364	2	Q6MB12	Q6mb12 parachlamyd
1142	75.5	5.4	368	2	Q85GC4	Q85gc4 abelia chin
1143	75.5	5.4	370	2	Q6D6F2	Q6d6f2 erwinia car
1144	75.5	5.4	379	2	Q6WRG7	Q6wrg7 bolomys tem
1145	75.5	5.4	383	2	Q7QT54	Q7qt54 giardia lam
1146	75.5	5.4	387	2	Q6FBC4	Q6fbc4 acinetobact
1147	75.5	5.4	388	2	Q6ML49	Q6ml49 bdellovibri
1148	75.5	5.4	396	2	Q7WTF8	Q7wtf8 streptomyce
1149	75.5	5.4	397	2	Q27976	Q27976 archaeoglob
1150	75.5	5.4	403	2	Q8RJL1	Q8rjl1 vibrio chol
1151	75.5	5.4	406	2	Q75D62	Q75d62 ashbya goss
1152	75.5	5.4	409	2	Q6PNA8	Q6pna8 steinernema
1153	75.5	5.4	419	2	Q734Y3	Q734y3 bacillus ce
1154	75.5	5.4	425	2	Q9BK21	Q9bk21 caenorhabdi
1155	75.5	5.4	432	1	RFBX_SALTI	Q99191 salmonella
1156	75.5	5.4	439	2	Q8S3C1	Q8s3c1 thraustochy
1157	75.5	5.4	441	2	Q59179	Q59179 pyrococcus
1158	75.5	5.4	445	2	Q81S42	Q81s42 bacillus an
1159	75.5	5.4	452	1	YEEF_ECOLI	P33016 escherichia
1160	75.5	5.4	452	2	Q65LZ3	Q65l23 bacillus li
1161	75.5	5.4	452	2	Q83R09	Q83r09 shigella fl
1162	75.5	5.4	454	2	Q8XFX1	Q8xfj1 salmonella
1163	75.5	5.4	454	2	Q7CQB1	Q7cqb1 salmonella
1164	75.5	5.4	454	2	Q8FG56	Q8fg56 escherichia
1165	75.5	5.4	457	2	Q8FHA4	Q8fha4 escherichia
1166	75.5	5.4	459	1	TCR_STAAU	P02983 staphylococ
1167	75.5	5.4	459	1	TCR_STAEP	P62967 staphylococ
1168	75.5	5.4	470	2	Q9KJV1	Q9kjl1 lactobacill
1169	75.5	5.4	476	1	MELB_SALTY	P30878 salmonella
1170	75.5	5.4	480	2	Q6APZ6	Q6apz6 desulfotale
1171	75.5	5.4	492	2	Q8Z5H6	Q8z5h6 salmonella
1172	75.5	5.4	492	2	Q9F798	Q9f798 salmonella
1173	75.5	5.4	494	2	Q67NV0	Q67nv0 symbiobacte
1174	75.5	5.4	498	2	Q9ZHR7	Q9zhr7 azospirillu
1175	75.5	5.4	499	2	Q8ZM30	Q8zm30 salmonella
1176	75.5	5.4	510	2	Q6GPO3	Q6gpq3 xenopus lae
1177	75.5	5.4	513	1	MEMP_ALCEU	Q07252 alcaligenes
1178	75.5	5.4	514	2	Q7N8B5	Q7n8b5 photorhabdu
1179	75.5	5.4	518	2	Q74283	Q74283 coprinus ci
1180	75.5	5.4	519	2	Q9FCP1	Q9fcp1 rhizobium l
1181	75.5	5.4	531	2	Q8EZV0	Q8ezv0 leptospira
1182	75.5	5.4	532	2	Q30727	Q30727 rhodobacter
1183	75.5	5.4	532	2	Q930J1	Q930j1 rhizobium m
1184	75.5	5.4	536	2	Q8SUS1	Q8sus1 encephalito
1185	75.5	5.4	540	2	Q65G56	Q65g56 bacillus li
1186	75.5	5.4	567	1	DSBD_CAMJTE	Q9phr3 campylobact
1187	75.5	5.4	571	2	Q7MJS9	Q7mjs9 vibrio vuln
1188	75.5	5.4	607	2	Q8SEE1	Q8see1 trichosurus
1189	75.5	5.4	632	2	Q6BXV6	Q6bxv6 debaryomyce
1190	75.5	5.4	638	2	Q81LF4	Q81lf4 bacillus an
1191	75.5	5.4	646	2	Q65D41	Q65d41 bacillus li
1192	75.5	5.4	652	2	Q8WH42	Q8wh42 leptaulus c
1193	75.5	5.4	655	2	Q7NC25	Q7nc25 mycoplasma
1194	75.5	5.4	671	2	Q9TJU2	Q9tju2 danais xant
1195	75.5	5.4	672	2	Q8HUS4	Q8hus4 Jaimehinton
1196	75.5	5.4	676	1	CCMF_RHIME	P45404 rhizobium m
1197	75.5	5.4	679	2	Q8WGU3	Q8wgu3 pennantia c
1198	75.5	5.4	696	2	Q9THQ0	Q9thq0 emmenanthe
1199	75.5	5.4	696	2	Q9TIW3	Q9tiw3 romanzoffia

1200	75.5	5.4	696	2	Q9TIW6	Q9tiw6 phacelia pa
1201	75.5	5.4	696	2	Q9TIY4	Q9tiy4 phacelia bo
1202	75.5	5.4	698	2	Q8MGG4	Q8mgg4 acanthocaly
1203	75.5	5.4	699	2	Q6PF58	Q6ff58 acinetobact
1204	75.5	5.4	703	2	Q8WH66	Q8wh66 hebenstreti
1205	75.5	5.4	703	2	Q8WH98	Q8wh98 dischisma c
1206	75.5	5.4	717	2	Q8FRN3	Q8frn3 corynebacte
1207	75.5	5.4	725	2	Q8M981	Q8m981 polyosma cu
1208	75.5	5.4	732	2	Q9TJS5	Q9tjs5 pseudomussa
1209	75.5	5.4	732	2	Q9TJT9	Q9tjt9 emmenoptery
1210	75.5	5.4	735	2	Q9SKA9	Q9ska9 arabisidopsis
1211	75.5	5.4	738	2	Q8WGU0	Q8wgu0 polyosma cu
1212	75.5	5.4	740	2	Q19944	Q19944 hebenstreti
1213	75.5	5.4	741	2	Q71QW4	Q71qw4 riencourtia
1214	75.5	5.4	741	2	Q71QX0	Q71qx0 polymnia ca
1215	75.5	5.4	746	2	Q9TL45	Q9tl45 syringa emo
1216	75.5	5.4	832	1	NAH3_RABIT	P26432 oryctolagus
1217	75.5	5.4	839	1	NAH3_DIDMA	Q28362 didelphis m
1218	75.5	5.4	870	2	Q69YG8	Q69yg8 homo sapien
1219	75.5	5.4	914	1	PBPA_BACSU	P39793 bacillus su
1220	75.5	5.4	932	2	O01623	O01623 caenorhabdi
1221	75.5	5.4	935	2	Q7M7P8	Q7m7p8 wolinnella s
1222	75.5	5.4	995	2	Q7SEV7	Q7sev7 neurospora
1223	75.5	5.4	999	1	PHAB_RHIME	Q52978 rhizobium m
1224	75.5	5.4	1040	2	Q8A203	Q8a203 bacteroides
1225	75.5	5.4	1046	2	Q68441	Q68441 agrobacteri
1226	75.5	5.4	1094	2	Q7Q5Q3	Q7q5q3 anopheles g
1227	75.5	5.4	1471	2	Q651S5	Q651s5 oryza sativ
1228	75.5	5.4	2180	2	Q7R1F8	Q7r1f8 giardia lam
1229	75	5.4	121	2	Q8EUK8	Q8euk8 mycoplasma
1230	75	5.4	161	2	Q6A5R2	Q6a5r2 propionibac
1231	75	5.4	193	2	Q6KDE2	Q6kde2 escherichia
1232	75	5.4	194	2	Q8FJ03	Q8fj03 escherichia
1233	75	5.4	208	2	Q7VDU9	Q7vdu9 prochloroco
1234	75	5.4	214	2	Q96L02	Q96l02 homo sapien
1235	75	5.4	231	2	Q88FH8	Q88fh8 pseudomonas
1236	75	5.4	240	2	Q81N55	Q81n55 bacillus an
1237	75	5.4	262	2	Q7NBJ4	Q7nbj4 mycoplasma
1238	75	5.4	262	2	Q9KD01	Q9kd01 bacillus ha
1239	75	5.4	282	2	Q7PBQ2	Q7pbq2 rickettsia
1240	75	5.4	286	2	Q8CTA7	Q8cta7 staphylococ
1241	75	5.4	289	2	O04409	O04409 phaseolus v
1242	75	5.4	290	1	RBN_SALTY	Q8zkt5 salmonella
1243	75	5.4	291	2	P93435	P93435 oryza sativ
1244	75	5.4	292	1	LICB_HAEIN	P14182 haemophilus
1245	75	5.4	295	2	Q7YFS3	Q7yfs3 neivamyrmex
1246	75	5.4	295	2	Q7YFT0	Q7yft0 eciton burc
1247	75	5.4	295	2	Q7YFT4	Q7yft4 eciton mexi
1248	75	5.4	298	2	Q55473	Q55473 synechocyst
1249	75	5.4	299	2	Q7P2A8	Q7p2a8 fusobacteri
1250	75	5.4	302	2	Q8U0A1	Q8u0a1 pyrococcus
1251	75	5.4	316	2	Q7VDF3	Q7vdf3 prochloroco
1252	75	5.4	321	2	Q85J72	Q85j72 varanus sal
1253	75	5.4	322	2	Q8U7S7	Q8u7s7 agrobacteri
1254	75	5.4	339	2	Q8J1R6	Q8j1r6 saccharomyc
1255	75	5.4	360	2	Q739K7	Q739k7 bacillus ce
1256	75	5.4	381	2	Q715Y4	Q715y4 baiomys tay
1257	75	5.4	382	2	Q66SL8	Q66sl8 bipes trida
1258	75	5.4	394	1	CIW3_HUMAN	O14649 homo sapien
1259	75	5.4	395	1	CDSA_MYCPN	P75160 m putative
1260	75	5.4	398	2	O59482	O59482 pyrococcus
1261	75	5.4	398	2	Q8RMJ9	Q8rmj9 corynebacte
1262	75	5.4	403	2	Q8RJK4	Q8rjk4 vibrio chol
1263	75	5.4	429	1	ARSB_STAXY	Q01255 staphylococ
1264	75	5.4	430	2	Q65UU6	Q65uu6 mannheimia
1265	75	5.4	432	2	O58733	O58733 pyrococcus
1266	75	5.4	442	2	Q6L0Y3	Q6l0y3 picrophilus
1267	75	5.4	451	2	Q980K3	Q980k3 sulfolobus
1268	75	5.4	452	2	Q9VI79	Q9vi79 drosophila
1269	75	5.4	452	2	Q8RTV1	Q8rtv1 uncultured
1270	75	5.4	459	2	Q94WR0	Q94wr0 buteo buteo
1271	75	5.4	459	2	Q7SZW7	Q7szw7 brachydanio
1272	75	5.4	461	2	Q8VMX0	Q8vmx0 listeria mo

1273	75	5.4	461	2	Q8Y8Q8	Q8y8g8	listeria mo	1346	74.5	5.4	215	2	Q8XKC6	Q8xkc6	clostridium
1274	75	5.4	473	1	YIHO SALTY	Q917r4	salmonella	1347	74.5	5.4	235	2	Q8ZQP8	Q8zqp8	salmonella
1275	75	5.4	478	2	Q7ZVQ2	Q7zvg2	brachydanio	1348	74.5	5.4	246	2	Q7YBY0	Q7yby0	strongyloce
1276	75	5.4	480	2	Q6QT99	Q6qt99	trypanosoma	1349	74.5	5.4	255	2	Q71AR6	Q71ar6	psilodera a
1277	75	5.4	494	2	Q87S84	Q87s84	vibrio para	1350	74.5	5.4	261	2	Q8EAF3	Q8eaf3	shewanella
1278	75	5.4	494	2	Q9KU42	Q9ku42	vibrio chol	1351	74.5	5.4	265	2	Q8DFQ3	Q8dfq3	vibrio vuln
1279	75	5.4	495	2	Q7ML56	Q7ml56	vibrio vuln	1352	74.5	5.4	268	2	Q8NSY4	Q8nsy4	corynebacte
1280	75	5.4	497	2	Q7U357	Q7u357	bordetella	1353	74.5	5.4	271	2	Q7M8Y3	Q7m8y3	wolinella s
1281	75	5.4	502	2	Q93Z26	Q93z26	arabidopsis	1354	74.5	5.4	273	2	Q6SGH5	Q6sgh5	uncultured
1282	75	5.4	507	2	Q928S0	Q928s0	listeria in	1355	74.5	5.4	275	2	Q7MMN1	Q7mmn1	vibrio vuln
1283	75	5.4	522	1	NFF2 HUMAN	Q9y5x5	homo sapien	1356	74.5	5.4	288	2	O23771	O23771	craterostig
1284	75	5.4	528	2	Q6CME2	Q6cme2	kluuveromyc	1357	74.5	5.4	288	2	Q8BZP2	Q8bzip2	mus musculu
1285	75	5.4	528	2	Q7Z8R4	Q7z8r4	kluuveromyc	1358	74.5	5.4	293	2	Q8U855	Q8u855	agrobacteri
1286	75	5.4	540	2	Q7XA06	Q7xa06	arabidopsis	1359	74.5	5.4	297	2	Q9G226	Q9g226	rana sylvat
1287	75	5.4	540	2	Q6G1N2	Q6g1n2	bartonella	1360	74.5	5.4	301	2	Q88169	Q88169	enterococcu
1288	75	5.4	544	2	Q7RG44	Q7rg44	plasmodium	1361	74.5	5.4	302	2	Q832M6	Q832m6	enterococcu
1289	75	5.4	546	2	Q65NC0	Q65nc0	bacillus li	1362	74.5	5.4	304	2	Q8SKM6	Q8skm6	nitellopsis
1290	75	5.4	547	2	Q8FTZ4	Q8ftz4	corynebacte	1363	74.5	5.4	304	2	Q8SKM7	Q8skm7	lychnothamn
1291	75	5.4	551	1	FVR2 MOUSE	Q91x85	mus musculu	1364	74.5	5.4	304	2	Q8SKM8	Q8skm8	lamprothamn
1292	75	5.4	569	2	Q6XJN3	Q6xjn3	diploknema	1365	74.5	5.4	304	2	Q8SKM9	Q8skm9	chara conni
1293	75	5.4	570	2	Q6XJL4	Q6xjl4	mimusops co	1366	74.5	5.4	307	2	Q88EZ3	Q88ez3	pseudomonas
1294	75	5.4	573	2	Q6XJM5	Q6xjm5	labramia co	1367	74.5	5.4	311	2	O51622	O51622	borrelia bu
1295	75	5.4	573	2	Q7VMZ4	Q7vmz4	haemophilus	1368	74.5	5.4	313	2	Q86UH0	Q86uh0	homo sapien
1296	75	5.4	573	2	Q8EYE3	Q8eye3	leptospira	1369	74.5	5.4	316	2	Q7P2T9	Q7p2t9	fusobacteri
1297	75	5.4	576	2	Q6XJH2	Q6xjh2	tieghemella	1370	74.5	5.4	323	1	O16197	O16197	caenorhabdi
1298	75	5.4	580	2	Q6XJP8	Q6xjp8	autranella	1371	74.5	5.4	324	1	MRAY_BACSU	MRAY_BACSU	
1299	75	5.4	580	2	Q85MB6	Q85mb6	monoblephar	1372	74.5	5.4	324	2	Q8RXQ9	Q8rxq9	arabidopsis
1300	75	5.4	599	2	Q9LZD0	Q9lzd0	arabidopsis	1373	74.5	5.4	325	2	Q9PAR1	Q9par1	xylella fas
1301	75	5.4	624	1	COX1 BACPF	Q04440	bacillus ps	1374	74.5	5.4	325	2	Q6ARZ8	Q6arz8	desulfotale
1302	75	5.4	643	2	O29273	O29273	archaeoglob	1375	74.5	5.4	341	2	Q6NYV2	Q6nyv2	brachydanio
1303	75	5.4	650	2	Q8WH99	Q8wh99	discophora	1376	74.5	5.4	341	2	Q6UUV6	Q6ujv6	timaspis ph
1304	75	5.4	650	2	Q6MQ29	Q6mq29	bdellovibri	1377	74.5	5.4	359	2	Q8ZVW8	Q8zvw8	pyrobaculum
1305	75	5.4	656	2	Q6XJH1	Q6xjh1	vitellariop	1378	74.5	5.4	361	2	Q8KB33	Q8kb33	chlorobium
1306	75	5.4	658	2	Q6XJL3	Q6xjl3	sideroxylon	1379	74.5	5.4	362	2	Q9Z6R4	Q9z6r4	chlamydia p
1307	75	5.4	658	2	Q6XJK5	Q6xjk5	payena luci	1380	74.5	5.4	366	2	O36050	O36050	lamprothamn
1308	75	5.4	658	2	Q6XJK8	Q6xjk8	northea sey	1381	74.5	5.4	374	1	CIW9_HUMAN	CIW9_HUMAN	
1309	75	5.4	658	2	Q6XJL2	Q6xjl2	mimusops ze	1382	74.5	5.4	396	2	Q88H29	Q88hz9	pseudomonas
1310	75	5.4	658	2	Q6XJL3	Q6xjl3	mimusops el	1383	74.5	5.4	398	2	Q6A8D3	Q6a8d3	propionibac
1311	75	5.4	658	2	Q6XJM4	Q6xjm4	labramia ma	1384	74.5	5.4	399	2	O23485	O23485	caenorhabdi
1312	75	5.4	658	2	Q6XJM7	Q6xjm7	faucherea p	1385	74.5	5.4	400	2	Q688H5	Q688h5	oryza sativ
1313	75	5.4	665	2	Q7Q4E5	Q7q4e5	anopheles g	1386	74.5	5.4	405	2	Q924N0	Q924n0	mus musculu
1314	75	5.4	685	2	Q6C7G7	Q6c7g7	yarrowia li	1387	74.5	5.4	409	2	O06481	O06481	bacillus su
1315	75	5.4	693	2	Q31905	Q31905	borago offi	1388	74.5	5.4	410	2	Q6E8A0	Q6e8a0	erechtia sp
1316	75	5.4	696	2	Q9TIV0	Q9tiv0	phacelia mi	1389	74.5	5.4	411	2	P93390	P93390	nicotiana t
1317	75	5.4	696	2	Q9TIV3	Q9tiv3	nama serice	1390	74.5	5.4	414	2	Q638U4	Q638u4	bacillus ce
1318	75	5.4	699	2	Q9MU19	Q9mu19	martynia an	1391	74.5	5.4	415	2	Q94YV9	Q94yv9	timmia bava
1319	75	5.4	702	2	Q8WHC4	Q8whc4	solanum dip	1392	74.5	5.4	417	2	Q7YH69	Q7yh69	taenia asia
1320	75	5.4	705	2	Q6AP92	Q6ap92	desulfotale	1393	74.5	5.4	419	2	Q8R0P1	Q8r0p1	mus musculu
1321	75	5.4	743	2	Q9TLB0	Q9tlb0	nematanthus	1394	74.5	5.4	424	2	Q6F9T4	Q6f9t4	acinetobact
1322	75	5.4	754	2	Q7KWK4	Q7kwk4	dictyosteli	1395	74.5	5.4	426	2	Q6W2H2	Q6w2h2	rhizobium s
1323	75	5.4	820	2	Q9N429	Q9n429	caenorhabdi	1396	74.5	5.4	430	2	Q7TNE9	Q7tne9	mus musculu
1324	75	5.4	881	2	Q6FE07	Q6fe07	acinetobact	1397	74.5	5.4	430	2	Q9JK46	Q9jk46	mus musculu
1325	75	5.4	917	1	IL6B MOUSE	Q00560	mus musculu	1398	74.5	5.4	439	2	Q66DX3	Q66dx3	yersinia ps
1326	75	5.4	917	2	Q6PD19	Q6pd19	mus musculu	1399	74.5	5.4	439	2	Q8ZC24	Q8zc24	yersinia pe
1327	75	5.4	939	2	Q669T0	Q669t0	yersinia ps	1400	74.5	5.4	441	2	Q81YL5	Q81yl5	bacillus an
1328	75	5.4	1012	2	Q9SY16	Q9sy16	asterina pe	1401	74.5	5.4	441	2	Q6HFW1	Q6hfw1	bacillus th
1329	75	5.4	1047	2	Q7PNG3	Q7png3	anopheles g	1402	74.5	5.4	447	2	Q17837	Q17837	caenorhabdi
1330	75	5.4	1056	2	O22855	O22855	arabidopsis	1403	74.5	5.4	450	2	O27920	O27920	bradysia hy
1331	75	5.4	1065	2	Q8A6B8	Q8a6b8	bacteroides	1404	74.5	5.4	451	2	Q8MPG6	Q8mpg6	trypanosoma
1332	75	5.4	1115	2	Q7QSA8	Q7qsa8	giardia lam	1405	74.5	5.4	451	2	Q8K2E0	Q8k2e0	mus musculu
1333	75	5.4	1276	2	Q8MI49	Q8mi49	felis silve	1406	74.5	5.4	453	2	Q65DH6	Q65dh6	bacillus li
1334	75	5.4	1276	2	Q8MKD8	Q8mkd8	felis silve	1407	74.5	5.4	453	2	Q6LN43	Q6ln43	photobacter
1335	75	5.4	1280	2	Q95Y17	Q95yi7	asterina pe	1408	74.5	5.4	453	2	Q6CYX8	Q6cyx8	erwinia car
1336	75	5.4	1294	1	YOH5 YEAST	Q08234	saccharomyc	1409	74.5	5.4	454	2	Q83W84	Q83w84	escherichia
1337	75	5.4	1612	2	Q6PYX7	Q6pyx7	ostreococcu	1410	74.5	5.4	458	2	Q8CQF9	Q8cqf9	staphylococ
1338	75	5.4	1986	2	Q91UJ3	Q91uj3	aconitum la	1411	74.5	5.4	469	1	MELB_ECOLI	P02921	escherichia
1339	75	5.4	2183	2	Q6W9E8	Q6w9e8	human echov	1412	74.5	5.4	469	2	Q7UBB0	Q7ubb0	shigella fl
1340	74.5	5.4	128	2	Q631X7	Q631x7	bacillus ce	1413	74.5	5.4	469	2	Q8XDU0	Q8xd0	escherichia
1341	74.5	5.4	141	2	Q9ZQY8	Q9zqy8	arabidopsis	1414	74.5	5.4	471	2	Q81I29	Q81i29	bacillus ce
1342	74.5	5.4	174	2	Q97UA8	Q97ua8	sulfolobus	1415	74.5	5.4	472	2	Q66L46	Q66l46	mus musculu
1343	74.5	5.4	184	2	Q68J58	Q68js8	gopherus po	1416	74.5	5.4	476	2	Q8Z9R4	Q8z9r4	salmonella
1344	74.5	5.4	201	2	Q8K6L8	Q8k6l8	streptococc	1417	74.5	5.4	476	2	Q8ZS16	Q8zs16	salmonella
1345	74.5	5.4	202	2	Q7PHK7	Q7phk7	anopheles g	1418	74.5	5.4	480	2	Q65GD6	Q65gd6	bacillus li

1419 74.5 5.4 481 2 Q83PA7 Q83pa7 shigella fl
1420 74.5 5.4 482 2 Q93QW4 Q93qw4 bacteroides
1421 74.5 5.4 483 2 Q85MF0 Q85mf0 saliya bois
1422 74.5 5.4 488 2 Q6FA73 Q6fa73 acinetobact
1423 74.5 5.4 492 2 Q67LL3 Q67ll3 symbiobacte
1424 74.5 5.4 503 2 Q66IG1 Q66ig1 xenopus tro
1425 74.5 5.4 507 2 Q83W34 Q83w34 rickettsia
1426 74.5 5.4 529 1 G161 HUMAN Q8n6u8 homo sapien
1427 74.5 5.4 533 2 Q8K376 Q8k376 mus musculu
1428 74.5 5.4 535 2 Q84KR3 Q84kr3 oryza sativ
1429 74.5 5.4 535 2 Q69JW3 Q69jw3 oryza sativ
1430 74.5 5.4 544 2 O44965 O44965 caenorhabdi
1431 74.5 5.4 547 2 Q73WU9 Q73wu9 mycobacteri
1432 74.5 5.4 560 2 O44703 O44703 caenorhabdi
1433 74.5 5.4 564 2 Q6H9F4 Q6h9f4 monttea chi
1434 74.5 5.4 567 2 Q8BGX8 Q8bgx8 m mus muscu
1435 74.5 5.4 580 2 Q63EP4 Q63ep4 bacillus ce
1436 74.5 5.4 588 2 Q7XPE1 Q7xpe1 oryza sativ
1437 74.5 5.4 589 2 Q8X120 Q8xl20 exophiala d
1438 74.5 5.4 592 2 Q8BUR1 Q8bur1 mus musculu
1439 74.5 5.4 594 2 Q9GEW2 Q9gew2 coris monsp
1440 74.5 5.4 600 2 Q6EVN3 Q6evn3 lamprothamn
1441 74.5 5.4 606 2 Q86LG0 Q86lg0 drosophila
1442 74.5 5.4 610 2 Q70SP5 Q70sp5 limosella g
1443 74.5 5.4 612 2 Q76FH0 Q76fh0 auxis roche
1444 74.5 5.4 612 2 Q76G39 Q76g39 auxis roche
1445 74.5 5.4 612 2 Q8HKX9 Q8hcx9 pterocaesio
1446 74.5 5.4 616 2 Q7QWH6 Q7qwh6 giardia lam
1447 74.5 5.4 631 2 Q8THX4 Q8thx4 methanosarc
1448 74.5 5.4 633 1 PARE MYCGA Q59526 mycoplasma
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1450 74.5 5.4 646 2 Q8WH87 Q8wh87 emmotum nit
1451 74.5 5.4 647 2 Q9GEW3 Q9gew3 claviija eue
1452 74.5 5.4 663 2 Q98479 Q98479 'escallonia
1453 74.5 5.4 675 2 Q7YAM5 Q7yam5 chara vulga
1454 74.5 5.4 684 2 Q9TK71 Q9tk71 montia diff
1455 74.5 5.4 688 2 Q7YMI2 Q7ym12 brunfelsia
1456 74.5 5.4 690 2 Q9TIW4 Q9tiw4 hesperochir
1457 74.5 5.4 695 2 Q8WJY2 Q8wjy2 merxmuellet
1458 74.5 5.4 695 2 Q9TIT8 Q9tit8 eucrypta ch
1459 74.5 5.4 696 2 Q9TIT2 Q9tit2 phacelia ra
1460 74.5 5.4 697 2 Q8HTZ3 Q8htz3 anthocercis
1461 74.5 5.4 700 2 Q9TLG0 Q9tlg0 amphianthus
1462 74.5 5.4 701 2 Q9MVL7 Q9mv17 abutilon hy
1463 74.5 5.4 705 2 Q6E571 Q6e571 aureolaria
1464 74.5 5.4 714 2 Q9TK85 Q9tk85 alluaudia h
1465 74.5 5.4 726 2 Q19937 Q19937 emorya suav
1466 74.5 5.4 740 2 Q9MTR0 Q9mtr0 quintinia v
1467 74.5 5.4 741 2 Q71QU8 Q71qu8 tridax balb
1468 74.5 5.4 741 2 Q85Z03 Q85z03 stevia reba
1469 74.5 5.4 744 2 Q9MTR4 Q9mtr4 nephrophyll
1470 74.5 5.4 794 1 Y966 CORGL P35867 corynebacte
1471 74.5 5.4 799 2 Q75G84 Q75g84 oryza sativ
1472 74.5 5.4 804 2 Q7NLY9 Q7nly9 gloeobacter
1473 74.5 5.4 869 1 MUTS THETN Q8ra71 thermoanaer
1474 74.5 5.4 889 2 Q8YS17 Q8ys17 anabaena sp
1475 74.5 5.4 1118 2 Q65U88 Q65u88 mannheimia
1476 74.5 5.4 1124 2 Q86UF3 Q86uf3 homo sapien
1477 74.5 5.4 1132 2 Q7QZ72 Q7qz72 giardia lam
1478 74.5 5.4 1449 2 Q6AXE3 Q6axe3 mus musculu
1479 74 5.3 121 2 Q8W533 Q8w533 setaria ita
1480 74 5.3 212 2 Q6TGUS Q6tgu5 brachydanio
1481 74 5.3 212 2 Q7ZUB3 Q7zub3 brachydanio
1482 74 5.3 217 2 P70017 P70017 xenopus lae
1483 74 5.3 231 2 Q89265 Q89265 gallid herp
1484 74 5.3 231 2 Q782M9 Q782m9 gallid herp
1485 74 5.3 238 2 Q75204 Q75204 homo sapien
1486 74 5.3 238 2 Q8BGP5 Q8bgp5 m mus muscu
1487 74 5.3 242 2 Q48598 Q48598 lactococcus
1488 74 5.3 268 2 Q7YTL8 Q7ytl8 caenorhabdi
1489 74 5.3 271 2 Q94VC8 Q94vc8 varanus pil
1490 74 5.3 277 2 Q9Z779 Q9z779 chlamydia p
1491 74 5.3 281 2 Q97WM7 Q97wm7 sulfolobus

1492 74 5.3 295 2 Q7YFS7 Q7yfs7 nomamymex
1493 74 5.3 295 2 Q6CYN2 Q6cyn2 erwinia car
1494 74 5.3 295 2 Q7ZY07 Q7zy07 xenopus lae
1495 74 5.3 296 1 GLTR BACSU P94501 bacillus su
1496 74 5.3 300 2 Q6G458 Q6g458 bartonella
1497 74 5.3 303 2 O01459 O01459 caenorhabdi
1498 74 5.3 304 2 Q8DLR4 Q8dlr4 synechococc
1499 74 5.3 311 2 Q87MZ7 Q87mz7 vibrio para
1500 74 5.3 321 2 Q94VA9 Q94va9 varanus sal

ALIGNMENTS

RESULT 1

Q6UX65 PRELIMINARY; PRT; 266 AA.
ID Q6UX65
AC Q6UX65;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE WWFQ154.
GN ORFNames=UNQ154;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AY358492; AAQ8856.1; -.
SQ SEQUENCE 266 AA; 29766 MW; 4F91D5C212D458E5 CRC64;

Query Match 100.0%; Score 1392; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.2e-107;
Matches 266; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWWFQOGLSFLPSALVIWTSAAPIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWWFQOGLSFLPSALVIWTSAAPIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
QY 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
Db 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
QY 121 HVSGAVLTFGMGSLYMFVQITLSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSSVL 180
Db 121 HVSGAVLTFGMGSLYMFVQITLSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSSVL 180
QY 181 HSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFQKISLRVEAN 240
Db 181 HSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFLTYIRDFQKISLRVEAN 240
QY 241 LHGLTYDTAPCPINNERTRLLSRDI 266
Db 241 LHGLTYDTAPCPINNERTRLLSRDI 266

RESULT 2

Q9CR48

ID Q9CR48 PRELIMINARY; PRT; 267 AA.
AC Q9CR48;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:2610318G18 product:hypothetical protein, full
DE insert sequence (Mus musculus adult male tongue cDNA, RIKEN full-
DE length enriched library, clone:2310056E01 product:hypothetical
DE protein, full insert sequence) (Mus musculus 10 days lactation, adult
DE female mammary gland cDNA, RIKEN full-length enriched library,
DE clone:D730039I03 product:hypothetical protein, full insert
DE sequence).
GN Name=2610318G18Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue, and Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK012044; BAB27990.1; -.
DR EMBL; AK009940; BAB26598.1; -.
DR EMBL; AK052824; BAC35162.1; -.
DR MGD; MGI:1914421; 2610318G18Rik.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 30227 MW; 228214D5AFF36783 CRC64;

Query Match 89.4%; Score 1245; DB 2; Length 267;
Best Local Similarity 86.4%; Pred. No. 2e-95;
Matches 229; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MWVFOQGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWVFOQGLSFLPSALVIWTFATFIFSYITAITLHHVDPALPYISDTGTIPPERCLFGVML 60

Qy 61 NIAAVLCIATIVYRYKQVHALSPEENVIKLNKAGLVGLSCLGLSIVANFQKTLFAA 120
Db 61 NIAAVLGIATMYRYKQVHALNPEENLIKNKAGLVGLSCLGLSLVANFQKSTLFIV 120

Qy 121 HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSSVL 180
Db 121 HVCGAVLAFSMGSPYMFVQTILSYQMOPKIHKSQVFWVRLLLVTCGVSALSMTCSSIL 180

Qy 181 HSGNFGTDLEQKLHNWPNEDKGYVLHMTTAAEWSMSFSFFGFLTYIRDFOKISLRVEAN 240
Db 181 YSSDFGPDVVQKLHNWPNEDKGYVLHLVTTAAEWSMSFSFFGFLTYIRDFOKITLRVEAN 240

Qy 241 LHGLTLYDTAPCPINNERTLLSRD 265
Db 241 LHGLTLYDTVPCPVNNERTPLLSRD 265

RESULT 3
Q9D520
ID Q9D520 PRELIMINARY; PRT; 267 AA.
AC Q9D520;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4930524M19 product:hypothetical protein, full insert
DE sequence.
DE Name=2610318G18Rik;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";

Db 181 ANLHGLTLYDTAPCPINNERTRLLSRDI 208

RESULT 5

Q9D835 ID Q9D835 PRELIMINARY; PRT; 180 AA.

AC Q9D835;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Mus musculus adult male small intestine cDNA, RIKEN full-length

DE enriched library, clone:2010305N14 product:hypothetical protein, full

DE insert sequence (2610318G18Rik protein).

GN Name=2610318G18Rik;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RA The FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format

RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

RN [6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Small intestine;

RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBBJ databases.

RN [7]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [8]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Kidney;

RA Strausberg R.;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBBJ databases.

DR EMBL; AK008532; BAB25725.1; -.

DR EMBL; BC024458; AAH24458.1; -.

DR MGD; MGI:1914421; 2610318G18Rik.

KW Hypothetical protein.

SQ SEQUENCE 180 AA; 20324 MW; 7952C2302D9235DF CRC64;

Query Match 57.9%; Score 805.5; DB 2; Length 180;

Best Local Similarity 60.0%; Pred. No. 4.5e-59;

Matches 159; Conservative 12; Mismatches 7; Indels 87; Gaps 1;

Qy 1 MWMFQOGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

Db 1 MWMFQOGLSFLPSALVIWTFATFIFSYITAITLHVDPALPYISDTGTIPPERCLFGVML 60

Qy 61 NIAAVLCIATIVRYKQVHALSPEENVIIKLNKAGLVGLGILSCLGISIVANFQKTLFAA 120

Db 61 NIAAVLGIATMYRYKQVHALNPEENLIKLNKAGLVGLGILSCLGLSLVANFQ----- 113

Qy 121 HVSGAVLTFGMGSLYMFVQTILSYQMOPKIHKQVFWIRLLLVWCGVSALSMLTCSSVL 180

Db 114 ----- 113

Qy 181 HSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFOKISLRVEAN 240

Db 114 -----GYYVLHLVTTAAEWSMSFSFFGFFLTYYIRDFOKITLREAN 153

Qy 241 LHGLTLYDTAPCPINNERTRLLSRD 265

Db 154 LHGLTLYDTVPCPVNNERTPLLSRD 178

RESULT 6

Q6IQ10 ID Q6IQ10 PRELIMINARY; PRT; 272 AA.

AC Q6IQ10;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE zgc:86754.

GN ORFNames=zgc:86754;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071426; AAH71426.1; --
DR ZFIN; ZDB-GENE-040625-141; zgc:86754.
SQ SEQUENCE 272 AA; 30362 MW; B7FE8BDD89FC87FA CRC64;

Query Match 54.9%; Score 764.5; DB 2; Length 272;
Best Local Similarity 55.2%; Pred. No. 1.7e-55;
Matches 138; Conservative 48; Mismatches 63; Indels 1; Gaps 1;

QY 1 MWFFQQLSFLPSALVIWTSAAFIYSITATVTLHHIDPALPYISDTGTVAPEKCLFGAML 60
Db 1 MWFFQGLCVLPVALVWTAATFIFAYITAVVLRHVDPLVPYISDTGTVAPERCVFGVML 60

QY 61 NIAAVLCIATIVRYKQVHALSP-EENVIIKLNKAGLVGLISCLGLSIVANFOKTLFA 119
Db 61 NVSAFLGVAITMYRYKQLQALADVDDTRLNRLNVGVFVFGCCSFGMCVVANFOKTLFS 120

QY 120 AHVSGAVLTFMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSVV 179
Db 121 MHLVGAILTFGICALYVFIQTALSYLMQPHIHSKTMFWTRLSVGIWTLSSIIIMFVSSVI 180

QY 180 LHSGNFGTDLQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEA 239
Db 181 MYSTLPGVEVNNKLLHWTPGEPGFTAHIVSTISEWSLALSFSIFFLTYYIRDFKKNLRASA 240

QY 240 NLHGLTLYDT 249
Db 241 ELQSNHLYES 250

RESULT 7
Q8NBQ4 PRELIMINARY; PRT; 136 AA.
AC Q8NBQ4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein PSEC0031.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.,
RA Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
RA Nagahari K., Sugano S., Isogai T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075350; BAC11562.1; --
SQ SEQUENCE 136 AA; 15728 MW; 984FEDC29636ACOC CRC64;

Query Match 52.1%; Score 725; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 MGSLYNFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSVLSHSGNFGTDLE 190
Db 1 MGSLYNFVQTILSYQMOPKIHGKQVFWIRLLLVWCGVSALSMLTCSVLSHSGNFGTDLE 60

QY 191 QKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTA 250
Db 61 QKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYDTA 120

QY 251 PCPINNERTRLSRDI 266
Db 121 PCPINNERTRLSRDI 136

RESULT 8
Q8N682 PRELIMINARY; PRT; 238 AA.
AC Q8N682;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLJ11259 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018435; AAH18435.1; --
DR InterPro; IPR000504; RNA_rec_mot.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.

DR	PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.	RL	Genome Res. 10:1617-1630(2000).
SQ	SEQUENCE 238 AA; 26253 MW; 511875677737F6C0 CRC64;	RN	[5]
	Query Match 35.4%; Score 492.5; DB 2; Length 238;	RP	SEQUENCE FROM N.A.
	Best Local Similarity 38.8%; Pred. No. 6e-33;	RC	STRAIN=C57BL/6J; TISSUE=Lung;
	Matches 97; Conservative 53; Mismatches 79; Indels 21; Gaps 3;	RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Qy	1 MWFFQOGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60	RA	Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,
Db	1 MLCFLRGMAFVPFLLVTWSSAAFIISYVAVLSGHVNPFLPYISDTGTTTPESGIFGFM 60	RA	Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Qy	61 NIAAVLCIATYVRYKQV-----HALSPEENVIIKLNKAGLVGLSCLGLSIVANFQ 113	RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Db	61 NFSAFLGAATMYTRYKIVQKQNTCYFSTPVFNLV-----SLVLGLVCGFGMGIVANFQ 114	RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Qy	114 KTTLFAAHVSGAVLTFEGMGLSYMFVQTLISYQMQPKIHGKQVFWIRLLLVICGVSALS 173	RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Db	115 ELAVPVVHDGGALLAFVCGVVYTLQLQSIISYKSCPQWNSLTCHVRMAISAVSAAVPM 174	RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Qy	174 LTCSSVLHSGNFGTDLQKLNHNPEDKGYVLHMITTAAEWSMSFSFFGFELTYIRDFQKI 233	RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
Db	175 IVCASLISI-----TKLEWNPREDKYVYHVVSALCEWTVAFGFIFYFLTFIQDFQSV 226	RT	"RIKEN integrated sequence analysis (RISA) system-384-format
Qy	234 SLRVEANLHG 243	RL	sequencing pipeline with 384 multicapillary sequencer.";
Db	227 TLRISTEING 236	RN	Genome Res. 10:1757-1771(2000).
		RP	[6]
		RC	SEQUENCE FROM N.A.
		RA	STRAIN=C57BL/6J; TISSUE=Lung;
		RA	Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
		RA	Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
		RA	Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
		RA	Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
		RA	Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
		RA	Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
		RA	Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
		RA	Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
		RA	Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
		RA	Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
		RA	Muramatsu M., Hayashizaki Y.;
		RL	Submitted (JUL-2000) to the EMBL/GenBank/DBSJ databases.
		DR	EMBL; AK004552; BAB23366.2; --
		DR	MGD; MGI:1918962; 1200002N14Rik.
		DR	GO; GO:0016021; C:integral to membrane; TAS.
		DR	InterPro; IPR000504; RNA_rec_mot.
		DR	InterPro; IPR009058; Wing_hlx_DNA_bnd.
		DR	PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
		KW	Hypothetical protein.
		SQ	SEQUENCE 238 AA; 26200 MW; AC89F1301B0A0048 CRC64;
			Query Match 34.4%; Score 479.5; DB 2; Length 238;
			Best Local Similarity 37.3%; Pred. No. 7.3e-32;
			Matches 93; Conservative 56; Mismatches 79; Indels 21; Gaps 3;
Qy	1 MWFFQOGLSFLPSALVIWTSAAFIYSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60		
Db	1 MLCFLRGMAFVPFLLVTWSSAAFIISYVAVLSGHVNPFLPYISDTGTTTPESGIFGFM 60		
Qy	61 NIAAVLCIATYVRYKQV-----HALSPEENVIIKLNKAGLVGLSCLGLSIVANFQ 113		
Db	61 NFSAFLGAATMYTRYKIVEKQNETCYFSTPVFNLV-----SLALGLVCGICMGIVANFQ 114		
Qy	114 KTTLFAAHVSGAVLTFEGMGLSYMFVQTLISYQMQPKIHGKQVFWIRLLLVICGVSALS 173		
Db	115 ELAVPVVHDGGALLAFVCGVVYTLQLQSIISYKSCPQWNSLTCHVRMAISAVSAAVPM 174		
Qy	174 LTCSSVLHSGNFGTDLQKLNHNPEDKGYVLHMITTAAEWSMSFSFFGFELTYIRDFQKI 233		
Db	175 IACASLISI-----TKLEWNPKEKDYIYHVVSALCEWTVAFGFIFYFLTFIQDFQSV 226		
Qy	234 SLRVEANLH 242		
Db	227 TLRISTEIN 235		
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		DT	05-JUL-2004 (TrEMBLrel. 27, Created)
		DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
		DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
		DE	LOC431986 protein (Fragment).
		GN	Name=LOC431986;

QY	11	LPSALVWTSAAAFISYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIAT	70
Db	7	LPVLTFLIFQVTFGLGTIYFAVLEGHVVTVPYISDAATSPESCQVGLINIGSVLLGIT	66
QY	71	IYVRKYQVHAL--SPE-ENVIIKLNKAGLVGLISCLGLSIVANFQKTTLFAAHVSGAV	126
Db	67	IYVRYRQVLQYEHHPDLDSGLRQNRALWFLVSCLGISFVGNFQETNVRIVHFIGAF	126
QY	127	LTEGMSGLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICGVSALSML--TCSSVLHSG	183
Db	127	CCFGCGTLFYFMQALISYLIFPMSGTRINAHRLGMSVVCTILFILLAVTGVMSHILFKG	186
QY	184	NFGTDLEQKLHNWPNEDKGYVLHMITTAAEWSMSFSFFGFFELTYIRDFOKISL	235
Db	187	-----QNPWKWYPSDGGWYFHVSSISEWVIATVFSFFILSFTNEFRDVS	232

RESULT 14

Q86F93

PRELIMINARY;

PRT;

252 AA.

AC

Q86F93;

DT

01-JUN-2003 (TReMBLrel. 24, Created)

DT

01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT

01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE

Clone ZZZ42 mRNA sequence.

OS

Schistosoma japonicum (Blood fluke).

OC

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;

OC

Schistosomatoidea; Schistosomatidae; Schistosoma.

OX

NCBI_TaxID=6182;

RN

[1]

RP

SEQUENCE FROM N.A.

RX

MEDLINE=2287925; PubMed=12973349; DOI=10.1038/ngl1236;

RA

Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,

RA

Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,

RA

Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,

RA

Xue C.L., Feng Z., Chen Z., Han Z.G.;

RT

"Evolutionary and biomedical implications of a Schistosoma japonicum

RT

complementary DNA resource."

RL

Nat. Genet. 35:139-147(2003).

DR

EMBL; AY222970; AAP05982.1; -.

SQ

SEQUENCE 252 AA; 28444 MW; 64035F88E507B3F0 CRC64;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2005, 16:50:35 ; Search time 43 Seconds
(without alignments)
461.783 Million cell updates/sec

Title: US-10-006-867-2
Perfect score: 1392
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query Match	Length	DB ID	Description
		%				
1	1388	99.7	267	4	US-09-663-600A-190	Sequence 190, App
2	595.5	42.8	172	4	US-09-663-600A-96	Sequence 96, Appl
3	479.5	34.4	238	3	US-09-724-864-38	Sequence 38, Appl
4	358	25.7	69	4	US-09-663-600A-130	Sequence 130, App
5	358	25.7	69	4	US-09-663-600A-224	Sequence 224, App
6	118	8.5	21	3	US-08-905-223-20	Sequence 20, Appl
7	118	8.5	21	3	US-09-247-155-20	Sequence 20, Appl
8	118	8.5	21	4	US-09-663-600A-20	Sequence 20, Appl
9	118	8.5	21	4	US-09-621-976-2	Sequence 2, Appli
10	118	8.5	21	4	US-09-513-999C-2	Sequence 2, Appli
11	118	8.5	21	4	US-09-471-276-2	Sequence 2, Appli
12	91.5	6.6	291	4	US-09-107-532A-4147	Sequence 4147, Ap
13	91.5	6.6	387	4	US-09-721-870-14	Sequence 14, Appl
14	90	6.5	283	4	US-09-602-787A-588	Sequence 588, App
15	90	6.5	396	4	US-09-248-796A-20434	Sequence 20434, A
16	88	6.3	344	4	US-09-248-796A-16383	Sequence 16383, A
17	88	6.3	1165	1	US-08-240-357-2	Sequence 2, Appli
18	86.5	6.2	356	4	US-09-134-000C-4914	Sequence 4914, Ap
19	85.5	6.1	579	4	US-09-786-681A-4	Sequence 4, Appli
20	85.5	6.1	582	4	US-09-786-681A-2	Sequence 2, Appli
21	85	6.1	419	4	US-09-948-774-2	Sequence 2, Appli
22	85	6.1	1180	3	US-08-726-214-12	Sequence 12, Appl
23	84.5	6.1	296	4	US-09-134-000C-6205	Sequence 6205, Ap
24	84	6.0	241	4	US-09-328-352-8001	Sequence 8001, Ap
25	84	6.0	506	4	US-09-540-236-2605	Sequence 2605, Ap
26	84	6.0	537	4	US-09-489-039A-14149	Sequence 14149, A
27	84	6.0	602	4	US-09-252-991A-22527	Sequence 22527, A

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38	82	5.9	474	4	US-09-252-991A-30354	Sequence 30354, A
39	82	5.9	574	4	US-09-248-796A-20154	Sequence 20154, A
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41	82	5.9	1094	4	US-09-949-016-8755	Sequence 8755, Ap
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48	81.5	5.9	208	4	US-09-107-433-4691	Sequence 4691, Ap
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52	81	5.8	425	4	US-09-489-039A-8209	Sequence 8209, Ap
53	80.5	5.8	298	4	US-09-489-039A-11920	Sequence 11920, A
54	80.5	5.8	359	4	US-09-828-523A-14	Sequence 14, Appl
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56	80.5	5.8	411	3	US-09-134-001C-3299	Sequence 3299, Ap
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74	79	5.7	298	4	US-09-438-185A-545	Sequence 545, App
75	79	5.7	491	4	US-09-543-681A-4195	Sequence 4195, Ap
76	79	5.7	600	4	US-09-134-000C-5694	Sequence 5694, Ap
77	79	5.7	670	4	US-09-489-039A-7251	Sequence 7251, Ap
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80	78.5	5.6	832	3	US-09-097-053-12	Sequence 12, Appl
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91	77	5.5	385	4	US-09-540-236-3736	Sequence 3736, Ap
92	77	5.5	506	4	US-09-719-919A-1	Sequence 1, Appli
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102	76	5.5	378	4	US-09-107-532A-6500	Sequence 6500, Ap	175	73.5	5.3	630	1	US-07-959-943-9	Sequence 9, Appli
103	76	5.5	424	4	US-09-252-991A-18895	Sequence 18895, A	176	73.5	5.3	693	4	US-09-252-991A-19167	Sequence 19167, A
104	76	5.5	429	4	US-09-922-501-10	Sequence 10, Appl	177	73.5	5.3	717	4	US-09-134-000C-5833	Sequence 5833, Ap
105	76	5.5	435	6	5268463-9	Patent No. 5268463	178	73.5	5.3	1099	3	US-08-726-214-14	Sequence 14, Appl
106	76	5.5	435	6	5268463-9	Patent No. 5268463	179	73.5	5.3	2020	1	US-07-551-531-2	Sequence 2, Appli
107	76	5.5	453	4	US-09-252-991A-17394	Sequence 17394, A	180	73.5	5.3	2485	5	PCT-US94-00198-1	Sequence 1, Appli
108	76	5.5	633	4	US-09-949-016-10337	Sequence 10337, A	181	73.5	5.3	2485	5	PCT-US94-00198-2	Sequence 2, Appli
109	75.5	5.4	313	4	US-09-252-991A-27163	Sequence 27163, A	182	73.5	5.3	2818	1	US-08-510-284-1	Sequence 1, Appli
110	75.5	5.4	401	4	US-09-489-039A-11546	Sequence 11546, A	183	73.5	5.3	2818	1	US-08-411-389-2	Sequence 2, Appli
111	75.5	5.4	445	4	US-09-328-352-6669	Sequence 6669, Ap	184	73.5	5.3	2818	2	US-08-449-933-2	Sequence 2, Appli
112	75.5	5.4	517	4	US-09-248-796A-20437	Sequence 20437, A	185	73.5	5.3	2818	3	US-07-966-049A-2	Sequence 2, Appli
113	75.5	5.4	1155	4	US-09-543-681A-6286	Sequence 6286, Ap	186	73.5	5.3	2818	3	US-09-542-331-2	Sequence 2, Appli
114	75.5	5.4	1172	4	US-09-328-352-6071	Sequence 6071, Ap	187	73.5	5.3	2818	3	US-09-510-791-2	Sequence 2, Appli
115	75	5.4	218	4	US-09-328-352-5215	Sequence 5215, Ap	188	73	5.2	178	4	US-09-328-352-5593	Sequence 5593, Ap
116	75	5.4	283	4	US-09-107-433-3024	Sequence 3024, Ap	189	73	5.2	187	4	US-09-328-352-7918	Sequence 7918, Ap
117	75	5.4	290	3	US-09-134-001C-4893	Sequence 4893, Ap	190	73	5.2	234	4	US-09-270-767-45527	Sequence 45527, A
118	75	5.4	344	1	US-08-689-974-1	Sequence 1, Appli	191	73	5.2	291	4	US-09-252-991A-32938	Sequence 32938, A
119	75	5.4	344	3	US-09-058-376-1	Sequence 1, Appli	192	73	5.2	431	4	US-09-710-279-2566	Sequence 2566, Ap
120	75	5.4	394	3	US-09-144-914-4	Sequence 4, Appli	193	73	5.2	434	4	US-09-328-352-7304	Sequence 7304, Ap
121	75	5.4	399	4	US-09-489-039A-9414	Sequence 9414, Ap	194	73	5.2	445	2	US-08-900-148-2	Sequence 2, Appli
122	75	5.4	408	4	US-09-719-088B-2	Sequence 2, Appli	195	73	5.2	466	3	US-09-134-001C-3355	Sequence 3355, Ap
123	75	5.4	420	3	US-09-255-368-6	Sequence 6, Appli	196	73	5.2	727	4	US-09-815-923-10	Sequence 10, Appl
124	75	5.4	420	4	US-09-405-558-6	Sequence 6, Appli	197	73	5.2	3079	5	PCT-US94-00198-4	Sequence 4, Appli
125	75	5.4	457	4	US-09-489-039A-8037	Sequence 8037, Ap	198	72.5	5.2	227	4	US-09-583-110-3621	Sequence 3621, Ap
126	75	5.4	524	4	US-09-248-796A-20256	Sequence 20256, A	199	72.5	5.2	281	4	US-09-540-236-2349	Sequence 2349, Ap
127	75	5.4	579	4	US-09-720-317A-4	Sequence 4, Appli	200	72.5	5.2	319	4	US-09-543-681A-5398	Sequence 5398, Ap
128	74.5	5.4	304	4	US-09-328-352-6459	Sequence 6459, Ap	201	72.5	5.2	389	4	US-09-328-352-5055	Sequence 5055, Ap
129	74.5	5.4	321	4	US-09-252-991A-31084	Sequence 31084, A	202	72.5	5.2	413	4	US-09-540-236-3672	Sequence 3672, Ap
130	74.5	5.4	340	4	US-09-543-681A-5778	Sequence 5778, Ap	203	72.5	5.2	519	4	US-09-489-039A-13346	Sequence 13346, A
131	74.5	5.4	367	4	US-09-198-452A-1069	Sequence 1069, Ap	204	72.5	5.2	519	4	US-09-248-796A-20368	Sequence 20368, A
132	74.5	5.4	367	4	US-09-438-185A-996	Sequence 996, App	205	72.5	5.2	607	4	US-09-328-352-5096	Sequence 5096, Ap
133	74.5	5.4	384	4	US-09-248-796A-20119	Sequence 20119, A	206	72	5.2	261	4	US-09-538-092-318	Sequence 318, App
134	74.5	5.4	388	4	US-09-949-016-7631	Sequence 7631, Ap	207	72	5.2	273	4	US-09-328-352-5843	Sequence 5843, Ap
135	74.5	5.4	405	4	US-09-719-088B-3	Sequence 3, Appli	208	72	5.2	337	4	US-09-902-540-13005	Sequence 13005, A
136	74.5	5.4	407	4	US-09-364-425B-23	Sequence 23, Appl	209	72	5.2	355	4	US-09-170-496D-2	Sequence 2, Appli
137	74.5	5.4	436	6	5432081-10	Patent No. 5432081	210	72	5.2	430	3	US-09-134-001C-2981	Sequence 2981, Ap
138	74.5	5.4	436	6	5432081-10	Patent No. 5432081	211	72	5.2	468	4	US-09-543-681A-4671	Sequence 4671, Ap
139	74.5	5.4	443	4	US-09-328-352-7069	Sequence 7069, Ap	212	72	5.2	495	4	US-09-359-167-4	Sequence 4, Appli
140	74.5	5.4	475	4	US-09-248-796A-20067	Sequence 20067, A	213	72	5.2	502	4	US-09-579-250-12	Sequence 12, Appl
141	74.5	5.4	556	4	US-09-248-796A-20229	Sequence 20229, A	214	72	5.2	502	4	US-09-579-250-14	Sequence 14, Appl
142	74.5	5.4	601	1	US-08-194-338-2	Sequence 2, Appli	215	72	5.2	506	4	US-09-252-991A-25852	Sequence 25852, A
143	74.5	5.4	1798	4	US-09-270-767-60233	Sequence 60233, A	216	72	5.2	569	2	US-08-750-723A-2	Sequence 2, Appli
144	74.5	5.4	2410	4	US-09-270-767-44775	Sequence 44775, A	217	72	5.2	569	3	US-09-191-275-2	Sequence 2, Appli
145	74	5.3	173	4	US-09-252-991A-22033	Sequence 22033, A	218	72	5.2	906	1	US-08-190-802A-31	Sequence 31, Appl
146	74	5.3	262	4	US-09-328-352-6026	Sequence 6026, Ap	219	72	5.2	906	3	US-08-477-346-31	Sequence 31, Appl
147	74	5.3	280	4	US-09-198-452A-889	Sequence 889, App	220	72	5.2	906	3	US-08-473-089-31	Sequence 31, Appl
148	74	5.3	280	4	US-09-438-185A-829	Sequence 829, App	221	72	5.2	906	4	US-08-487-072A-31	Sequence 31, Appl
149	74	5.3	282	4	US-09-583-110-3219	Sequence 3219, Ap	222	71.5	5.1	229	3	US-09-227-357-237	Sequence 237, App
150	74	5.3	292	2	US-09-024-848-2	Sequence 2, Appli	223	71.5	5.1	237	2	US-08-818-514-3	Sequence 3, Appli
151	74	5.3	292	3	US-09-348-116A-2	Sequence 2, Appli	224	71.5	5.1	237	3	US-09-115-934A-3	Sequence 3, Appli
152	74	5.3	332	4	US-09-902-540-15291	Sequence 15291, A	225	71.5	5.1	237	4	US-09-611-175-3	Sequence 3, Appli
153	74	5.3	445	4	US-08-937-834-5	Sequence 5, Appli	226	71.5	5.1	287	3	US-09-134-001C-5055	Sequence 5055, Ap
154	74	5.3	448	4	US-09-543-681A-7245	Sequence 7245, Ap	227	71.5	5.1	292	4	US-09-489-039A-12212	Sequence 12212, A
155	74	5.3	487	4	US-09-949-016-9649	Sequence 9649, Ap	228	71.5	5.1	372	2	US-08-501-003A-12	Sequence 12, Appl
156	74	5.3	727	4	US-09-543-681A-7968	Sequence 7968, Ap	229	71.5	5.1	379	3	US-09-740-035-4	Sequence 4, Appli
157	74	5.3	800	3	US-09-134-001C-5655	Sequence 5655, Ap	230	71.5	5.1	383	2	US-08-501-003A-14	Sequence 14, Appl
158	73.5	5.3	297	4	US-09-489-039A-8466	Sequence 8466, Ap	231	71.5	5.1	389	2	US-08-501-003A-11	Sequence 11, Appl
159	73.5	5.3	360	1	US-08-597-236-11	Sequence 11, Appl	232	71.5	5.1	391	2	US-08-501-003A-13	Sequence 13, Appl
160	73.5	5.3	360	1	US-08-746-682A-11	Sequence 11, Appl	233	71.5	5.1	391	4	US-09-949-016-5904	Sequence 5904, Ap
161	73.5	5.3	391	1	US-07-921-178A-2	Sequence 2, Appli	234	71.5	5.1	398	2	US-08-501-003A-15	Sequence 15, Appl
162	73.5	5.3	391	1	US-08-103-445-5	Sequence 5, Appli	235	71.5	5.1	411	4	US-09-949-016-8100	Sequence 8100, Ap
163	73.5	5.3	391	1	US-08-461-690B-5	Sequence 5, Appli	236	71.5	5.1	412	4	US-10-138-701-59	Sequence 59, Appl
164	73.5	5.3	391	2	US-08-501-003A-16	Sequence 16, Appl	237	71.5	5.1	484	4	US-09-248-796A-20357	Sequence 20357, A
165	73.5	5.3	391	4	US-09-543-681A-8292	Sequence 8292, Ap	238	71.5	5.1	519	4	US-09-198-452A-561	Sequence 561, App
166	73.5	5.3	391	4	US-09-275-252A-13	Sequence 13, Appl	239	71.5	5.1	521	4	US-09-438-185A-523	Sequence 523, App
167	73.5	5.3	395	4	US-09-489-039A-12123	Sequence 12123, A	240	71.5	5.1	535	4	US-09-252-991A-21652	Sequence 21652, A
168	73.5	5.3	416	4	US-09-543-681A-5455	Sequence 5455, Ap	241	71.5	5.1	552	4	US-09-270-767-45540	Sequence 45540, A
169	73.5	5.3	417	4	US-09-107-532A-4001	Sequence 4001, Ap	242	71.5	5.1	574	4	US-09-248-796A-20132	Sequence 20132, A
170	73.5	5.3	428	4	US-09-198-452A-720	Sequence 720, App	243	71.5	5.1	587	4	US-08-635-552A-3	Sequence 3, Appli
171	73.5	5.3	428	4	US-09-438-185A-682	Sequence 682, App	244	71	5.1	201	4	US-09-270-767-33463	Sequence 33463, A
172	73.5	5.3	514	4	US-09-489-039A-11902	Sequence 11902, A	245	71	5.1	201	4	US-09-270-767-48680	Sequence 48680, A
173	73.5	5.3	564	4	US-09-902-540-16018	Sequence 16018, A	246	71	5.1	332	4	US-09-313-942-10	Sequence 10, Appl

247	71	5.1	369	4	US-09-838-955A-3	Sequence 3, Appli	320	70	5.0	535	4	US-09-252-991A-21805	Sequence 21805, A
248	71	5.1	384	4	US-09-902-540-11956	Sequence 11956, A	321	70	5.0	539	4	US-09-538-092-741	Sequence 741, App
249	71	5.1	388	4	US-09-222-938A-37	Sequence 37, Appl	322	70	5.0	594	4	US-09-489-039A-10622	Sequence 10622, A
250	71	5.1	397	4	US-09-583-110-2946	Sequence 2946, Ap	323	70	5.0	688	4	US-09-438-185A-870	Sequence 870, App
251	71	5.1	404	4	US-09-107-433-3747	Sequence 3747, Ap	324	70	5.0	708	1	US-07-797-556-2	Sequence 2, Appli
252	71	5.1	408	4	US-09-489-039A-9583	Sequence 9583, Ap	325	70	5.0	708	1	US-08-308-881-2	Sequence 2, Appli
253	71	5.1	454	4	US-09-489-847-305	Sequence 305, App	326	70	5.0	708	2	US-09-058-263-2	Sequence 2, Appli
254	71	5.1	461	4	US-09-043-944-1	Sequence 1, Appli	327	70	5.0	708	2	US-09-059-099-2	Sequence 2, Appli
255	71	5.1	461	4	US-09-043-944-6	Sequence 6, Appli	328	70	5.0	708	3	US-09-058-264-2	Sequence 2, Appli
256	71	5.1	465	4	US-09-710-279-1676	Sequence 1676, Ap	329	70	5.0	708	4	US-09-455-962-2	Sequence 2, Appli
257	71	5.1	466	4	US-09-328-352-7117	Sequence 7117, Ap	330	70	5.0	708	5	PCT-US95-06530-2	Sequence 2, Appli
258	71	5.1	502	1	US-08-278-635B-7	Sequence 7, Appli	331	70	5.0	1028	4	US-09-328-352-5749	Sequence 5749, Ap
259	71	5.1	502	2	US-08-466-589-8	Sequence 8, Appli	332	70	5.0	1165	4	US-09-949-016-6874	Sequence 6874, Ap
260	71	5.1	502	2	US-08-700-636-8	Sequence 8, Appli	333	70	5.0	1165	4	US-09-949-016-11392	Sequence 11392, A
261	71	5.1	502	3	US-08-464-258B-7	Sequence 7, Appli	334	70	5.0	2105	2	US-08-808-793-3	Sequence 3, Appli
262	71	5.1	502	3	US-08-467-574-8	Sequence 8, Appli	335	70	5.0	2105	3	US-08-772-512A-3	Sequence 3, Appli
263	71	5.1	502	3	US-08-471-961-7	Sequence 7, Appli	336	70	5.0	2105	4	US-09-428-371-3	Sequence 3, Appli
264	71	5.1	502	3	US-09-217-345-8	Sequence 8, Appli	337	69.5	5.0	293	4	US-09-902-540-11200	Sequence 11200, A
265	71	5.1	502	4	US-08-487-596-12	Sequence 12, Appl	338	69.5	5.0	308	4	US-09-595-386-3	Sequence 3, Appli
266	71	5.1	502	4	US-09-345-109C-7	Sequence 7, Appli	339	69.5	5.0	308	4	US-09-993-525-3	Sequence 3, Appli
267	71	5.1	502	4	US-09-892-985-8	Sequence 8, Appli	340	69.5	5.0	345	4	US-09-543-681A-7546	Sequence 7546, Ap
268	71	5.1	502	4	US-09-579-250-2	Sequence 2, Appli	341	69.5	5.0	350	4	US-09-540-236-2338	Sequence 2338, Ap
269	71	5.1	502	4	US-09-579-250-10	Sequence 10, Appl	342	69.5	5.0	406	4	US-09-328-352-7149	Sequence 7149, Ap
270	71	5.1	571	4	US-09-252-991A-28549	Sequence 28549, A	343	69.5	5.0	417	4	US-09-405-558-44	Sequence 44, Appl
271	71	5.1	594	4	US-09-650-324A-59	Sequence 59, Appl	344	69.5	5.0	456	4	US-09-489-039A-8332	Sequence 8332, Ap
272	71	5.1	627	4	US-09-902-540-15743	Sequence 15743, A	345	69.5	5.0	460	4	US-09-489-039A-13505	Sequence 13505, A
273	71	5.1	658	2	US-08-825-558-4	Sequence 4, Appli	346	69.5	5.0	493	1	US-08-362-512A-4	Sequence 4, Appli
274	71	5.1	658	3	US-09-312-611-4	Sequence 4, Appli	347	69.5	5.0	493	3	US-08-964-939-4	Sequence 4, Appli
275	71	5.1	859	4	US-09-313-942-7	Sequence 7, Appli	348	69.5	5.0	493	4	US-09-854-774-4	Sequence 4, Appli
276	71	5.1	918	2	US-08-825-558-6	Sequence 6, Appli	349	69.5	5.0	501	4	US-09-252-991A-28456	Sequence 28456, A
277	71	5.1	918	3	US-09-312-611-6	Sequence 6, Appli	350	69.5	5.0	513	2	US-09-122-230-7	Sequence 7, Appli
278	71	5.1	918	4	US-09-853-180B-3	Sequence 3, Appli	351	69.5	5.0	530	4	US-09-540-236-2483	Sequence 2483, Ap
279	71	5.1	922	4	US-09-569-611C-41	Sequence 41, Appl	352	69.5	5.0	591	4	US-09-643-657-15	Sequence 15, Appl
280	71	5.1	951	4	US-09-313-942-9	Sequence 9, Appli	353	69.5	5.0	627	4	US-09-538-092-760	Sequence 760, App
281	71	5.1	971	4	US-09-868-572A-1	Sequence 1, Appli	354	69.5	5.0	653	1	US-07-782-298-2	Sequence 2, Appli
282	70.5	5.1	150	4	US-09-134-000C-4337	Sequence 4337, Ap	355	69.5	5.0	688	4	US-09-543-681A-4896	Sequence 4896, Ap
283	70.5	5.1	286	4	US-09-248-796A-17897	Sequence 17897, A	356	69.5	5.0	1277	3	US-09-397-885-3	Sequence 3, Appli
284	70.5	5.1	319	3	US-09-130-749-2	Sequence 2, Appli	357	69.5	5.0	1277	4	US-09-969-362-3	Sequence 3, Appli
285	70.5	5.1	319	3	US-09-170-496D-60	Sequence 60, Appl	358	69	5.0	114	3	US-09-134-001C-3376	Sequence 3376, Ap
286	70.5	5.1	319	4	US-09-949-016-10000	Sequence 10000, A	359	69	5.0	241	4	US-09-328-352-7032	Sequence 7032, Ap
287	70.5	5.1	386	4	US-09-949-016-10000	Sequence 10000, A	360	69	5.0	292	4	US-09-270-767-41753	Sequence 41753, A
288	70.5	5.1	387	4	US-09-489-039A-12240	Sequence 12240, A	361	69	5.0	293	4	US-09-438-185A-313	Sequence 313, App
289	70.5	5.1	395	4	US-09-543-681A-6203	Sequence 6203, Ap	362	69	5.0	294	4	US-09-902-540-11124	Sequence 11124, A
290	70.5	5.1	399	4	US-09-489-039A-8272	Sequence 8272, Ap	363	69	5.0	308	4	US-09-198-452A-606	Sequence 606, App
291	70.5	5.1	420	3	US-09-134-001C-3805	Sequence 3805, Ap	364	69	5.0	308	4	US-09-438-185A-569	Sequence 569, App
292	70.5	5.1	443	4	US-09-489-039A-8166	Sequence 8166, Ap	365	69	5.0	316	2	US-08-827-291A-2	Sequence 2, Appli
293	70.5	5.1	444	4	US-09-328-352-5249	Sequence 5249, Ap	366	69	5.0	344	4	US-10-121-757B-20	Sequence 20, Appl
294	70.5	5.1	454	2	US-08-748-485-1	Sequence 1, Appli	367	69	5.0	380	1	US-08-227-108-16	Sequence 16, Appl
295	70.5	5.1	467	4	US-09-107-532A-6175	Sequence 6175, Ap	368	69	5.0	380	2	US-09-073-674-16	Sequence 16, Appl
296	70.5	5.1	472	4	US-09-934-899-10	Sequence 10, Appl	369	69	5.0	380	2	US-09-328-352-7357	Sequence 7357, Ap
297	70.5	5.1	472	4	US-09-934-868-30	Sequence 30, Appl	370	69	5.0	403	4	US-09-489-039A-9921	Sequence 9921, Ap
298	70.5	5.1	473	4	US-09-949-016-11735	Sequence 11735, A	371	69	5.0	420	4	US-09-328-352-5907	Sequence 5907, Ap
299	70.5	5.1	474	4	US-09-486-192-4	Sequence 4, Appli	372	69	5.0	446	4	US-09-248-796A-20349	Sequence 20349, A
300	70.5	5.1	500	4	US-09-489-039A-10995	Sequence 10995, A	373	69	5.0	483	4	US-09-134-000C-4234	Sequence 4234, Ap
301	70.5	5.1	619	4	US-09-248-796A-20837	Sequence 20837, A	374	69	5.0	506	4	US-09-540-236-2360	Sequence 2360, Ap
302	70.5	5.1	669	4	US-09-949-016-6720	Sequence 6720, Ap	375	69	5.0	520	4	US-09-248-796A-20803	Sequence 20803, A
303	70.5	5.1	681	4	US-09-248-796A-20121	Sequence 20121, A	376	69	5.0	583	4	US-09-489-039A-13918	Sequence 13918, A
304	70.5	5.1	877	1	US-08-072-574-12	Sequence 12, Appl	377	69	5.0	642	4	US-09-252-991A-23588	Sequence 23588, A
305	70.5	5.1	955	4	US-09-252-991A-18882	Sequence 18882, A	378	69	5.0	719	4	US-09-328-352-6274	Sequence 6274, Ap
306	70.5	5.1	1134	3	US-08-726-214-2	Sequence 2, Appli	379	69	5.0	854	3	US-09-254-352B-18	Sequence 18, Appl
307	70.5	5.1	1134	4	US-09-245-039-2	Sequence 2, Appli	380	69	5.0	934	1	US-08-215-805A-80	Sequence 80, Appl
308	70.5	5.1	1788	2	US-08-962-284-2	Sequence 2, Appli	381	69	5.0	1095	3	US-09-112-096-15	Sequence 15, Appl
309	70	5.0	139	4	US-09-489-039A-8585	Sequence 8585, Ap	382	69	5.0	1095	4	US-09-636-215-778	Sequence 778, App
310	70	5.0	235	4	US-09-252-991A-19945	Sequence 19945, A	383	69	5.0	1095	4	US-09-685-166A-778	Sequence 778, App
311	70	5.0	296	4	US-09-328-352-7482	Sequence 7482, Ap	384	69	5.0	1095	4	US-09-679-426-778	Sequence 778, App
312	70	5.0	314	4	US-09-543-681A-6497	Sequence 6497, Ap	385	69	5.0	1095	4	US-09-759-143-778	Sequence 778, App
313	70	5.0	429	3	US-09-156-809-1	Sequence 1, Appli	386	69	5.0	1095	4	US-09-651-236-778	Sequence 778, App
314	70	5.0	429	4	US-10-006-915-1	Sequence 1, Appli	387	69	5.0	1180	1	US-08-072-574-8	Sequence 8, Appli
315	70	5.0	492	4	US-09-328-352-6875	Sequence 6875, Ap	388	69	5.0	1212	1	US-08-072-574-10	Sequence 10, Appl
316	70	5.0	496	4	US-09-489-039A-8772	Sequence 8772, Ap	389	69	5.0	2037	4	US-09-543-681A-5538	Sequence 5538, Ap
317	70	5.0	502	3	US-08-771-737-2	Sequence 2, Appli	390	69	5.0	2873	1	US-08-466-033-15	Sequence 15, Appl
318	70	5.0	502	4	US-09-954-936-2	Sequence 2, Appli	391	69	5.0	2873	1	US-08-638-911A-2	Sequence 2, Appli
319	70	5.0	526	4	US-09-543-681A-6494	Sequence 6494, Ap	392	69	5.0	2873	2	US-08-444-733-15	Sequence 15, Appl

393	69	5.0	2873	2	US-08-464-134-15	Sequence 15, Appl	466	67.5	4.8	317	4	US-09-489-039A-9602	Sequence 9602, Ap
394	69	5.0	2873	2	US-08-461-361-15	Sequence 15, Appl	467	67.5	4.8	323	4	US-09-107-532A-5460	Sequence 5460, Ap
395	69	5.0	2873	2	US-08-485-910-15	Sequence 15, Appl	468	67.5	4.8	327	4	US-09-543-681A-6219	Sequence 6219, Ap
396	69	5.0	2873	5	PCT-US95-06266-15	Sequence 15, Appl	469	67.5	4.8	336	1	US-08-332-312-4	Sequence 4, Appli
397	68.5	4.9	180	4	US-09-270-767-32589	Sequence 32589, A	470	67.5	4.8	360	4	US-09-949-016-10048	Sequence 10048, A
398	68.5	4.9	180	4	US-09-270-767-47806	Sequence 47806, A	471	67.5	4.8	411	4	US-09-328-352-5039	Sequence 5039, Ap
399	68.5	4.9	241	2	US-08-825-781-3	Sequence 3, Appli	472	67.5	4.8	421	4	US-09-198-452A-932	Sequence 932, App
400	68.5	4.9	264	3	US-09-724-864-64	Sequence 64, Appl	473	67.5	4.8	421	4	US-09-438-185A-869	Sequence 869, App
401	68.5	4.9	300	4	US-09-489-039A-10701	Sequence 10701, A	474	67.5	4.8	425	4	US-09-134-000C-5971	Sequence 5971, Ap
402	68.5	4.9	365	4	US-09-902-540-14946	Sequence 14946, A	475	67.5	4.8	484	4	US-09-252-991A-32299	Sequence 32299, A
403	68.5	4.9	396	4	US-09-107-532A-4277	Sequence 4277, Ap	476	67.5	4.8	536	4	US-09-107-532A-5507	Sequence 5507, Ap
404	68.5	4.9	400	3	US-09-134-001C-2912	Sequence 2912, Ap	477	67.5	4.8	586	4	US-09-252-991A-24994	Sequence 24994, A
405	68.5	4.9	405	4	US-09-543-681A-6109	Sequence 6109, Ap	478	67.5	4.8	612	4	US-09-248-796A-18040	Sequence 18040, A
406	68.5	4.9	412	3	US-09-134-001C-4885	Sequence 4885, Ap	479	67.5	4.8	625	4	US-09-902-540-15330	Sequence 15330, A
407	68.5	4.9	427	4	US-09-252-991A-29948	Sequence 29948, A	480	67.5	4.8	632	4	US-09-949-016-10386	Sequence 10386, A
408	68.5	4.9	428	4	US-09-328-352-5543	Sequence 5543, Ap	481	67.5	4.8	662	4	US-09-583-110-5119	Sequence 5119, Ap
409	68.5	4.9	459	4	US-09-583-110-5017	Sequence 5017, Ap	482	67.5	4.8	664	4	US-09-107-433-2775	Sequence 2775, Ap
410	68.5	4.9	465	4	US-09-489-039A-7435	Sequence 7435, Ap	483	67.5	4.8	667	1	US-07-879-617A-8	Sequence 8, Appli
411	68.5	4.9	470	4	US-09-107-433-4341	Sequence 4341, Ap	484	67.5	4.8	667	1	US-08-753-985-8	Sequence 8, Appli
412	68.5	4.9	480	4	US-09-305-681-2	Sequence 2, Appli	485	67.5	4.8	680	4	US-09-720-317A-18	Sequence 18, Appl
413	68.5	4.9	511	4	US-09-305-681-6	Sequence 6, Appli	486	67.5	4.8	693	4	US-09-949-016-9666	Sequence 9666, Ap
414	68.5	4.9	538	4	US-09-252-991A-23060	Sequence 23060, A	487	67.5	4.8	767	4	US-09-328-352-4613	Sequence 4613, Ap
415	68.5	4.9	541	4	US-09-976-594-931	Sequence 931, App	488	67.5	4.8	912	3	US-08-617-785-2	Sequence 2, Appli
416	68.5	4.9	549	4	US-09-248-796A-20436	Sequence 20436, A	489	67.5	4.8	912	3	US-09-641-318-2	Sequence 2, Appli
417	68.5	4.9	1091	3	US-09-306-595C-7	Sequence 7, Appli	490	67.5	4.8	912	4	US-09-817-464-2	Sequence 8, Appli
418	68.5	4.9	1091	4	US-09-925-388-7	Sequence 7, Appli	491	67.5	4.8	940	4	US-09-328-352-8165	Sequence 8, Appli
419	68.5	4.9	2104	2	US-08-808-793-4	Sequence 4, Appli	492	67.5	4.8	1084	4	US-09-221-013A-8	Sequence 8, Appli
420	68.5	4.9	2104	3	US-08-772-512A-4	Sequence 4, Appli	493	67.5	4.8	1326	4	US-09-328-352-4886	Sequence 4886, Ap
421	68.5	4.9	2104	4	US-09-428-371-4	Sequence 4, Appli	494	67	4.8	148	4	US-09-270-767-39883	Sequence 39883, A
422	68.5	4.9	3559	4	US-09-693-205A-10	Sequence 10, Appl	495	67	4.8	148	4	US-09-270-767-55100	Sequence 55100, A
423	68	4.9	253	3	US-08-858-207A-299	Sequence 299, App	496	67	4.8	162	4	US-09-270-767-45268	Sequence 45268, A
424	68	4.9	279	4	US-09-602-787A-658	Sequence 658, App	497	67	4.8	184	4	US-09-795-926-46	Sequence 46, Appl
425	68	4.9	309	4	US-09-710-279-42	Sequence 42, Appl	498	67	4.8	205	4	US-09-252-991A-28363	Sequence 28363, A
426	68	4.9	313	4	US-09-583-110-4236	Sequence 4236, Ap	499	67	4.8	217	4	US-09-134-000C-6287	Sequence 6287, Ap
427	68	4.9	315	4	US-09-107-433-3706	Sequence 3706, Ap	500	67	4.8	225	4	US-09-543-681A-7698	Sequence 7698, Ap
428	68	4.9	355	4	US-09-826-509-475	Sequence 475, App	501	67	4.8	277	4	US-09-489-039A-10481	Sequence 10481, A
429	68	4.9	379	4	US-09-252-991A-27854	Sequence 27854, A	502	67	4.8	290	4	US-09-248-796A-20347	Sequence 20347, A
430	68	4.9	404	4	US-09-328-352-8182	Sequence 8182, Ap	503	67	4.8	306	4	US-09-489-039A-10023	Sequence 10023, A
431	68	4.9	466	4	US-09-603-208A-236	Sequence 236, App	504	67	4.8	326	4	US-09-543-681A-6673	Sequence 6673, Ap
432	68	4.9	470	4	US-09-328-352-6673	Sequence 6673, Ap	505	67	4.8	345	4	US-09-248-796A-20118	Sequence 20118, A
433	68	4.9	476	4	US-09-328-352-6735	Sequence 6735, Ap	506	67	4.8	359	4	US-09-425-488-2	Sequence 2, Appli
434	68	4.9	484	3	US-09-134-001C-5063	Sequence 5063, Ap	507	67	4.8	360	4	US-09-489-039A-8125	Sequence 8125, Ap
435	68	4.9	486	3	US-09-134-001C-3593	Sequence 3593, Ap	508	67	4.8	375	4	US-09-543-681A-4465	Sequence 4465, Ap
436	68	4.9	503	4	US-09-248-796A-16650	Sequence 16650, A	509	67	4.8	382	4	US-09-489-039A-10783	Sequence 10783, A
437	68	4.9	548	4	US-09-328-352-6605	Sequence 6605, Ap	510	67	4.8	414	3	US-09-334-601-4	Sequence 4, Appli
438	68	4.9	605	4	US-09-583-110-4773	Sequence 4773, Ap	511	67	4.8	453	1	US-08-439-131A-5	Sequence 5, Appli
439	68	4.9	619	4	US-09-540-236-2377	Sequence 2377, Ap	512	67	4.8	453	1	US-08-440-674-4	Sequence 4, Appli
440	68	4.9	633	4	US-09-328-352-5439	Sequence 5439, Ap	513	67	4.8	453	4	US-08-879-337-6	Sequence 6, Appli
441	68	4.9	638	1	US-08-295-814E-13	Sequence 13, Appl	514	67	4.8	459	3	US-09-097-889-22	Sequence 22, Appl
442	68	4.9	638	1	US-08-240-783B-2	Sequence 2, Appli	515	67	4.8	459	4	US-09-098-079-22	Sequence 22, Appl
443	68	4.9	638	3	US-09-084-813-2	Sequence 2, Appli	516	67	4.8	465	4	US-09-252-991A-19135	Sequence 19135, A
444	68	4.9	638	3	US-09-343-361-13	Sequence 13, Appl	517	67	4.8	482	4	US-09-489-039A-9369	Sequence 9369, Ap
445	68	4.9	638	5	PCT-US92-09662-2	Sequence 2, Appli	518	67	4.8	490	4	US-09-328-352-5310	Sequence 5310, Ap
446	68	4.9	640	3	US-09-627-376-16	Sequence 16, Appl	519	67	4.8	494	4	US-09-489-039A-8154	Sequence 8154, Ap
447	68	4.9	640	4	US-10-047-676B-16	Sequence 16, Appl	520	67	4.8	505	4	US-09-328-352-7155	Sequence 7155, Ap
448	68	4.9	672	4	US-09-543-681A-5976	Sequence 5976, Ap	521	67	4.8	506	4	US-09-134-000C-6170	Sequence 6170, Ap
449	68	4.9	694	4	US-09-248-796A-20210	Sequence 20210, A	522	67	4.8	519	4	US-09-719-919A-17	Sequence 17, Appl
450	68	4.9	727	4	US-09-543-681A-6690	Sequence 6690, Ap	523	67	4.8	541	4	US-09-716-129-54	Sequence 54, Appl
451	68	4.9	783	4	US-09-165-396-2	Sequence 2, Appli	524	67	4.8	545	4	US-09-902-540-10576	Sequence 10576, A
452	68	4.9	905	4	US-09-538-092-1079	Sequence 1079, Ap	525	67	4.8	548	4	US-09-543-681A-4994	Sequence 4994, Ap
453	68	4.9	1024	4	US-09-562-737-87	Sequence 87, Appl	526	67	4.8	576	4	US-09-540-236-2286	Sequence 2286, Ap
454	68	4.9	2864	4	US-08-469-260A-394	Sequence 394, App	527	67	4.8	590	4	US-09-902-540-14944	Sequence 14944, A
455	68	4.9	2864	4	US-08-488-446-394	Sequence 394, App	528	67	4.8	601	4	US-09-134-000C-5783	Sequence 5783, Ap
456	68	4.9	2864	4	US-08-467-344A-394	Sequence 394, App	529	67	4.8	768	4	US-09-489-039A-12897	Sequence 12897, A
457	68	4.9	2864	4	US-08-424-550B-394	Sequence 394, App	530	67	4.8	774	4	US-09-328-352-5361	Sequence 5361, Ap
458	67.5	4.8	181	4	US-09-270-767-33574	Sequence 33574, A	531	67	4.8	1439	2	US-08-449-644-2	Sequence 2, Appli
459	67.5	4.8	196	3	US-09-383-586-11	Sequence 11, Appl	532	67	4.8	1439	2	US-08-087-244A-2	Sequence 2, Appli
460	67.5	4.8	196	4	US-09-823-038A-11	Sequence 11, Appl	533	67	4.8	1457	2	US-08-652-971-3	Sequence 3, Appli
461	67.5	4.8	240	4	US-09-540-236-2487	Sequence 2487, Ap	534	67	4.8	1457	2	US-08-449-644-1	Sequence 1, Appli
462	67.5	4.8	249	4	US-09-949-016-7192	Sequence 7192, Ap	535	67	4.8	1457	2	US-08-087-244A-1	Sequence 1, Appli
463	67.5	4.8	264	4	US-09-270-767-41787	Sequence 41787, A	536	67	4.8	1457	2	US-08-991-258A-3	Sequence 3, Appli
464	67.5	4.8	265	4	US-09-248-796A-17984	Sequence 17984, A	537	67	4.8	1457	2	US-08-769-399-3	Sequence 3, Appli
465	67.5	4.8	304	4	US-09-328-352-6103	Sequence 6103, Ap	538	67	4.8	1457	3	US-08-991-953A-3	Sequence 3, Appli

539	66.5	4.8	175	4	US-09-583-110-4664	Sequence 4664, Ap	612	66	4.7	483	4	US-09-107-532A-4123	Sequence 4123, Ap
540	66.5	4.8	179	4	US-09-107-433-4882	Sequence 4882, Ap	613	66	4.7	486	4	US-09-489-039A-7706	Sequence 7706, Ap
541	66.5	4.8	243	3	US-09-134-001C-4114	Sequence 4114, Ap	614	66	4.7	508	4	US-09-328-352-6467	Sequence 6467, Ap
542	66.5	4.8	249	3	US-08-858-207A-309	Sequence 309, App	615	66	4.7	511	1	US-08-278-635B-8	Sequence 8, Appli
543	66.5	4.8	249	4	US-09-270-767-38186	Sequence 38186, A	616	66	4.7	511	3	US-08-464-258B-8	Sequence 8, Appli
544	66.5	4.8	249	4	US-09-270-767-53403	Sequence 53403, A	617	66	4.7	511	3	US-08-471-961-8	Sequence 8, Appli
545	66.5	4.8	256	4	US-09-489-039A-9057	Sequence 9057, Ap	618	66	4.7	511	4	US-09-345-109C-8	Sequence 8, Appli
546	66.5	4.8	300	4	US-09-393-634-19	Sequence 19, Appl	619	66	4.7	536	4	US-09-270-767-44004	Sequence 44004, A
547	66.5	4.8	319	4	US-09-170-496D-196	Sequence 196, App	620	66	4.7	619	4	US-09-578-441-3	Sequence 3, Appli
548	66.5	4.8	324	4	US-09-543-681A-6241	Sequence 6241, Ap	621	66	4.7	620	4	US-09-578-441-4	Sequence 4, Appli
549	66.5	4.8	343	4	US-09-543-681A-6853	Sequence 6853, Ap	622	66	4.7	639	3	US-09-134-001C-5661	Sequence 5661, Ap
550	66.5	4.8	349	4	US-09-491-577-96	Sequence 96, Appl	623	66	4.7	687	3	US-08-834-467-2	Sequence 2, Appli
551	66.5	4.8	380	4	US-09-949-016-10856	Sequence 10856, A	624	66	4.7	687	3	US-09-396-177-2	Sequence 2, Appli
552	66.5	4.8	392	4	US-09-603-208A-134	Sequence 134, App	625	66	4.7	687	4	US-09-248-796A-14715	Sequence 14715, A
553	66.5	4.8	412	4	US-09-710-279-368	Sequence 368, App	626	66	4.7	748	4	US-09-902-540-13877	Sequence 13877, A
554	66.5	4.8	415	4	US-09-489-039A-10457	Sequence 10457, A	627	66	4.7	986	4	US-09-248-796A-19088	Sequence 19088, A
555	66.5	4.8	425	4	US-09-543-681A-7042	Sequence 7042, Ap	628	66	4.7	1216	4	US-09-248-796A-19646	Sequence 19646, A
556	66.5	4.8	444	4	US-09-694-519-6	Sequence 6, Appli	629	66	4.7	4377	4	US-09-949-016-6978	Sequence 6978, Ap
557	66.5	4.8	456	4	US-09-328-352-5446	Sequence 5446, Ap	630	65.5	4.7	157	4	US-09-461-325-155	Sequence 155, App
558	66.5	4.8	470	2	US-08-959-011-1	Sequence 1, Appli	631	65.5	4.7	157	4	US-10-112-542-155	Sequence 155, App
559	66.5	4.8	488	3	US-09-801-052-5	Sequence 5, Appli	632	65.5	4.7	157	4	US-10-115-123-155	Sequence 155, App
560	66.5	4.8	488	4	US-10-020-121-5	Sequence 5, Appli	633	65.5	4.7	160	4	US-09-270-767-46920	Sequence 46920, A
561	66.5	4.8	511	4	US-09-328-352-6365	Sequence 6365, Ap	634	65.5	4.7	195	4	US-09-489-039A-7897	Sequence 7897, Ap
562	66.5	4.8	515	4	US-09-489-039A-8402	Sequence 8402, Ap	635	65.5	4.7	267	4	US-09-198-452A-231	Sequence 231, App
563	66.5	4.8	525	4	US-09-252-991A-23870	Sequence 23870, A	636	65.5	4.7	270	4	US-09-270-767-44001	Sequence 44001, A
564	66.5	4.8	534	4	US-09-107-532A-6592	Sequence 6592, Ap	637	65.5	4.7	292	3	US-09-372-422A-4	Sequence 4, Appli
565	66.5	4.8	535	4	US-09-107-532A-7027	Sequence 6593, Ap	638	65.5	4.7	305	4	US-09-107-433-3400	Sequence 3400, Ap
566	66.5	4.8	536	4	US-09-809-665A-71	Sequence 71, Appl	639	65.5	4.7	310	4	US-09-328-352-8117	Sequence 8117, Ap
567	66.5	4.8	598	4	US-09-107-532A-7027	Sequence 7027, Ap	640	65.5	4.7	323	3	US-09-134-001C-4635	Sequence 4635, Ap
568	66.5	4.8	648	4	US-09-583-110-2729	Sequence 2729, Ap	641	65.5	4.7	329	3	US-09-740-035-2	Sequence 2, Appli
569	66.5	4.8	670	4	US-09-107-433-4919	Sequence 4919, Ap	642	65.5	4.7	329	4	US-09-710-279-1942	Sequence 1942, Ap
570	66.5	4.8	676	4	US-09-198-452A-836	Sequence 836, App	643	65.5	4.7	344	3	US-09-134-001C-5567	Sequence 5567, Ap
571	66.5	4.8	688	4	US-09-720-317A-2	Sequence 2, Appli	644	65.5	4.7	355	1	US-08-153-848-28	Sequence 28, Appl
572	66.5	4.8	719	4	US-09-438-185A-788	Sequence 788, App	645	65.5	4.7	355	1	US-08-153-848-32	Sequence 32, Appl
573	66.5	4.8	736	4	US-09-107-532A-6007	Sequence 6007, Ap	646	65.5	4.7	355	3	US-09-299-843A-28	Sequence 28, Appl
574	66.5	4.8	737	4	US-09-583-110-4038	Sequence 4038, Ap	647	65.5	4.7	355	3	US-09-299-843A-32	Sequence 32, Appl
575	66.5	4.8	738	4	US-09-328-352-4315	Sequence 4315, Ap	648	65.5	4.7	355	3	US-09-088-337B-28	Sequence 28, Appl
576	66.5	4.8	742	4	US-09-107-433-3626	Sequence 3626, Ap	649	65.5	4.7	355	3	US-09-088-337B-32	Sequence 32, Appl
577	66.5	4.8	755	4	US-09-489-039A-9089	Sequence 9089, Ap	650	65.5	4.7	355	4	US-09-170-496D-130	Sequence 130, App
578	66.5	4.8	865	4	US-09-252-991A-19339	Sequence 19339, A	651	65.5	4.7	355	4	US-09-170-496D-232	Sequence 232, App
579	66.5	4.8	899	4	US-09-437-568A-48	Sequence 48, Appl	652	65.5	4.7	355	4	US-09-917-254-68	Sequence 68, Appl
580	66.5	4.8	921	1	US-07-718-575-14	Sequence 14, Appl	653	65.5	4.7	355	5	PCT-US93-11153-28	Sequence 28, Appl
581	66.5	4.8	921	1	US-08-481-206-14	Sequence 14, Appl	654	65.5	4.7	355	5	PCT-US93-11153-32	Sequence 32, Appl
582	66.5	4.8	921	2	US-08-486-269A-14	Sequence 14, Appl	655	65.5	4.7	356	4	US-09-107-532A-4245	Sequence 4245, Ap
583	66.5	4.8	1059	4	US-10-160-719A-2	Sequence 2, Appli	656	65.5	4.7	391	4	US-09-107-532A-4209	Sequence 4209, Ap
584	66.5	4.8	1167	3	US-09-008-097-6	Sequence 6, Appli	657	65.5	4.7	391	4	US-09-543-681A-7029	Sequence 7029, Ap
585	66.5	4.8	1167	4	US-09-472-667-6	Sequence 6, Appli	658	65.5	4.7	391	4	US-09-248-796A-15698	Sequence 15698, A
586	66.5	4.8	1684	3	US-08-665-259-25	Sequence 25, Appl	659	65.5	4.7	393	4	US-09-351-150A-29	Sequence 29, Appl
587	66.5	4.8	1684	3	US-08-762-500-25	Sequence 25, Appl	660	65.5	4.7	399	4	US-09-328-352-8043	Sequence 8043, Ap
588	66.5	4.8	1704	3	US-08-762-500-75	Sequence 75, Appl	661	65.5	4.7	399	4	US-09-560-761B-4	Sequence 4, Appli
589	66.5	4.8	1704	4	US-09-032-438C-120	Sequence 120, App	662	65.5	4.7	422	4	US-09-809-665A-73	Sequence 73, Appl
590	66.5	4.8	1766	4	US-09-949-016-10796	Sequence 10796, A	663	65.5	4.7	426	6	5268463-8	Patent No. 5268463
591	66	4.7	171	3	US-09-107-383-16	Sequence 16, Appl	664	65.5	4.7	426	6	5268463-8	Patent No. 5268463
592	66	4.7	171	4	US-09-643-914-16	Sequence 16, Appl	665	65.5	4.7	427	4	US-09-438-185A-217	Sequence 217, App
593	66	4.7	171	4	US-09-742-361A-16	Sequence 16, Appl	666	65.5	4.7	428	1	US-08-570-157-5	Sequence 5, Appli
594	66	4.7	191	4	US-09-443-041A-24	Sequence 24, Appl	667	65.5	4.7	428	3	US-08-029-170-31	Sequence 31, Appl
595	66	4.7	254	4	US-09-902-540-15766	Sequence 15766, A	668	65.5	4.7	428	3	US-09-076-510-5	Sequence 5, Appli
596	66	4.7	260	4	US-09-443-041A-10	Sequence 10, Appl	669	65.5	4.7	428	4	US-09-004-349-5	Sequence 5, Appli
597	66	4.7	281	3	US-09-134-001C-4763	Sequence 4763, Ap	670	65.5	4.7	428	4	US-09-443-745-31	Sequence 31, Appl
598	66	4.7	345	4	US-09-252-991A-28113	Sequence 28113, A	671	65.5	4.7	437	4	US-09-489-039A-8958	Sequence 8958, Ap
599	66	4.7	355	2	US-08-846-762-93	Sequence 93, Appl	672	65.5	4.7	444	1	US-07-937-609-14	Sequence 14, Appl
600	66	4.7	367	3	US-09-134-001C-5557	Sequence 5557, Ap	673	65.5	4.7	444	3	US-08-029-170-14	Sequence 14, Appl
601	66	4.7	393	3	US-09-134-001C-5594	Sequence 5594, Ap	674	65.5	4.7	444	3	US-09-443-745-14	Sequence 14, Appl
602	66	4.7	400	4	US-09-198-452A-302	Sequence 302, App	675	65.5	4.7	457	2	US-08-882-704A-6	Sequence 6, Appli
603	66	4.7	400	4	US-09-438-185A-291	Sequence 291, App	676	65.5	4.7	457	4	US-09-151-957-6	Sequence 6, Appli
604	66	4.7	403	4	US-09-489-039A-11910	Sequence 11910, A	677	65.5	4.7	465	4	US-09-328-352-5222	Sequence 5222, Ap
605	66	4.7	415	3	US-09-080-044-6	Sequence 6, Appli	678	65.5	4.7	490	4	US-09-252-991A-27210	Sequence 27210, A
606	66	4.7	415	3	US-09-531-857A-6	Sequence 6, Appli	679	65.5	4.7	511	4	US-09-305-681-4	Sequence 4, Appli
607	66	4.7	431	5	PCT-US91-00909-6	Sequence 6, Appli	680	65.5	4.7	530	3	US-09-134-001C-4510	Sequence 4510, Ap
608	66	4.7	432	4	US-09-489-039A-7223	Sequence 7223, Ap	681	65.5	4.7	551	4	US-09-489-039A-9083	Sequence 9083, Ap
609	66	4.7	439	4	US-09-248-796A-20082	Sequence 20082, A	682	65.5	4.7	600	4	US-09-438-185A-1013	Sequence 1013, Ap
610	66	4.7	464	4	US-09-252-991A-18525	Sequence 18525, A	683	65.5	4.7	601	1	US-07-676-174A-2	Sequence 2, Appli
611	66	4.7	471	4	US-09-543-681A-5580	Sequence 5580, Ap	684	65.5	4.7	697	4	US-09-603-208A-226	Sequence 226, App

685	65.5	4.7	881	4	US-09-949-016-7764	Sequence 7764, Ap	758	65	4.7	541	3	US-08-888-077A-21	Sequence 21, Appl
686	65.5	4.7	908	3	US-08-855-146-2	Sequence 2, Appli	759	65	4.7	541	3	US-09-124-698-166	Sequence 166, App
687	65.5	4.7	1016	3	US-09-180-439-8	Sequence 8, Appli	760	65	4.7	541	3	US-09-127-480-166	Sequence 166, App
688	65.5	4.7	1036	2	US-08-720-824A-5	Sequence 5, Appli	761	65	4.7	541	3	US-09-124-523-166	Sequence 166, App
689	65.5	4.7	1036	3	US-08-953-823A-5	Sequence 5, Appli	762	65	4.7	541	4	US-09-636-796A-166	Sequence 166, App
690	65.5	4.7	1036	4	US-09-398-239-5	Sequence 5, Appli	763	65	4.7	541	4	US-09-949-016-11075	Sequence 11075, A
691	65.5	4.7	1036	4	US-09-560-876A-5	Sequence 5, Appli	764	65	4.7	545	4	US-09-198-452A-519	Sequence 519, App
692	65.5	4.7	1065	4	US-09-560-876A-6	Sequence 6, Appli	765	65	4.7	545	4	US-09-438-185A-483	Sequence 483, App
693	65	4.7	139	4	US-09-902-540-14543	Sequence 14543, A	766	65	4.7	562	4	US-09-328-352-4694	Sequence 4694, Ap
694	65	4.7	144	3	US-09-134-001C-3102	Sequence 3102, Ap	767	65	4.7	574	4	US-09-107-433-3877	Sequence 3877, Ap
695	65	4.7	154	4	US-09-955-732A-7	Sequence 7, Appli	768	65	4.7	599	1	US-08-222-619-2	Sequence 2, Appli
696	65	4.7	168	4	US-09-544-716-15	Sequence 15, Appl	769	65	4.7	599	3	US-08-221-767-24	Sequence 24, Appl
697	65	4.7	168	4	US-09-557-921-16	Sequence 16, Appl	770	65	4.7	599	5	PCT-US95-04075-2	Sequence 2, Appli
698	65	4.7	168	4	US-09-564-357-18	Sequence 18, Appl	771	65	4.7	633	4	US-09-248-796A-20407	Sequence 20407, A
699	65	4.7	168	4	US-09-619-380-17	Sequence 17, Appl	772	65	4.7	682	4	US-09-744-926-2	Sequence 2, Appli
700	65	4.7	198	3	US-09-213-293D-9	Sequence 9, Appli	773	65	4.7	738	4	US-09-107-532A-5096	Sequence 5096, Ap
701	65	4.7	202	4	US-09-107-433-3144	Sequence 3144, Ap	774	65	4.7	768	3	US-09-120-653D-5	Sequence 5, Appli
702	65	4.7	274	4	US-09-489-039A-14140	Sequence 14140, A	775	65	4.7	1095	4	US-09-636-215-780	Sequence 780, App
703	65	4.7	306	4	US-09-248-796A-17619	Sequence 17619, A	776	65	4.7	1095	4	US-09-685-166A-780	Sequence 780, App
704	65	4.7	313	2	US-08-990-379-7	Sequence 7, Appli	777	65	4.7	1095	4	US-09-679-426-780	Sequence 780, App
705	65	4.7	314	3	US-09-164-193-22	Sequence 22, Appl	778	65	4.7	1095	4	US-09-759-143-780	Sequence 780, App
706	65	4.7	314	4	US-09-221-448A-22	Sequence 22, Appl	779	65	4.7	1095	4	US-09-651-236-780	Sequence 780, App
707	65	4.7	315	4	US-09-393-634-56	Sequence 56, Appl	780	65	4.7	1104	4	US-09-793-998-11	Sequence 11, Appl
708	65	4.7	318	4	US-09-270-767-45996	Sequence 45996, A	781	65	4.7	3174	2	US-08-477-451-3	Sequence 3, Appli
709	65	4.7	331	4	US-09-252-991A-24546	Sequence 24546, A	782	64.5	4.6	173	4	US-09-270-767-33313	Sequence 33313, A
710	65	4.7	332	4	US-09-232-338-8	Sequence 8, Appli	783	64.5	4.6	173	4	US-09-270-767-48530	Sequence 48530, A
711	65	4.7	346	4	US-09-710-279-504	Sequence 504, App	784	64.5	4.6	238	3	US-09-134-001C-3136	Sequence 3136, Ap
712	65	4.7	356	4	US-09-107-532A-6286	Sequence 6286, Ap	785	64.5	4.6	240	4	US-09-543-681A-5483	Sequence 5483, Ap
713	65	4.7	367	4	US-09-252-991A-31459	Sequence 31459, A	786	64.5	4.6	259	4	US-09-489-039A-11949	Sequence 11949, A
714	65	4.7	371	4	US-09-540-236-3247	Sequence 3247, Ap	787	64.5	4.6	260	3	US-08-983-075D-9	Sequence 9, Appli
715	65	4.7	380	4	US-09-489-039A-8153	Sequence 8153, Ap	788	64.5	4.6	263	4	US-09-949-016-10927	Sequence 10927, A
716	65	4.7	383	4	US-09-710-279-2026	Sequence 2026, Ap	789	64.5	4.6	276	4	US-09-583-110-5031	Sequence 5031, Ap
717	65	4.7	387	4	US-09-710-279-3180	Sequence 3180, Ap	790	64.5	4.6	284	4	US-09-107-433-3147	Sequence 3147, Ap
718	65	4.7	390	4	US-09-710-279-1422	Sequence 1422, Ap	791	64.5	4.6	323	4	US-09-489-039A-7408	Sequence 7408, Ap
719	65	4.7	393	4	US-09-134-000C-4238	Sequence 4238, Ap	792	64.5	4.6	338	4	US-09-270-767-34974	Sequence 34974, A
720	65	4.7	404	4	US-09-710-279-1204	Sequence 1204, Ap	793	64.5	4.6	338	4	US-09-270-767-50191	Sequence 50191, A
721	65	4.7	405	4	US-09-543-681A-4311	Sequence 4311, Ap	794	64.5	4.6	344	4	US-08-311-731A-172	Sequence 172, App
722	65	4.7	406	3	US-09-134-001C-4084	Sequence 4084, Ap	795	64.5	4.6	381	4	US-09-248-796A-20097	Sequence 20097, A
723	65	4.7	415	3	US-09-134-001C-5101	Sequence 5101, Ap	796	64.5	4.6	398	4	US-09-348-930A-9	Sequence 9, Appli
724	65	4.7	423	4	US-09-824-551-2	Sequence 2, Appli	797	64.5	4.6	398	4	US-09-578-063-75	Sequence 75, Appl
725	65	4.7	426	4	US-09-252-991A-30025	Sequence 30025, A	798	64.5	4.6	399	4	US-09-328-352-7394	Sequence 7394, Ap
726	65	4.7	433	4	US-09-949-016-8065	Sequence 8065, Ap	799	64.5	4.6	404	4	US-09-489-039A-8947	Sequence 8947, Ap
727	65	4.7	436	4	US-09-583-110-4729	Sequence 4729, Ap	800	64.5	4.6	411	4	US-08-887-534A-80	Sequence 80, Appl
728	65	4.7	440	4	US-09-107-433-5201	Sequence 5201, Ap	801	64.5	4.6	411	4	US-09-527-431-80	Sequence 80, Appl
729	65	4.7	446	4	US-09-134-000C-6454	Sequence 6454, Ap	802	64.5	4.6	411	4	US-09-446-861-80	Sequence 80, Appl
730	65	4.7	459	4	US-09-489-039A-9027	Sequence 9027, Ap	803	64.5	4.6	412	4	US-09-198-452A-901	Sequence 901, App
731	65	4.7	472	4	US-09-489-039A-13479	Sequence 13479, A	804	64.5	4.6	413	4	US-09-438-185A-838	Sequence 838, App
732	65	4.7	482	4	US-09-902-540-10594	Sequence 10594, A	805	64.5	4.6	416	4	US-09-540-236-2393	Sequence 2393, Ap
733	65	4.7	490	3	US-09-134-001C-5116	Sequence 5116, Ap	806	64.5	4.6	436	4	US-09-949-016-11448	Sequence 11448, A
734	65	4.7	494	4	US-09-543-681A-7033	Sequence 7033, Ap	807	64.5	4.6	439	4	US-09-710-279-2408	Sequence 2408, Ap
735	65	4.7	503	3	US-09-134-001C-3096	Sequence 3096, Ap	808	64.5	4.6	459	3	US-09-134-001C-4856	Sequence 4856, Ap
736	65	4.7	505	4	US-09-134-000C-5340	Sequence 5340, Ap	809	64.5	4.6	462	4	US-09-902-540-10036	Sequence 10036, A
737	65	4.7	515	4	US-09-489-039A-12306	Sequence 12306, A	810	64.5	4.6	470	2	US-08-724-394A-10	Sequence 10, Appl
738	65	4.7	518	3	US-08-999-723-2	Sequence 2, Appli	811	64.5	4.6	493	4	US-09-489-039A-13709	Sequence 13709, A
739	65	4.7	518	3	US-09-434-427-2	Sequence 2, Appli	812	64.5	4.6	517	4	US-09-815-923-16	Sequence 16, Appl
740	65	4.7	518	4	US-09-548-372D-2	Sequence 2, Appli	813	64.5	4.6	534	4	US-09-252-991A-31719	Sequence 31719, A
741	65	4.7	518	4	US-09-548-367D-2	Sequence 2, Appli	814	64.5	4.6	539	4	US-09-518-959-8	Sequence 8, Appli
742	65	4.7	518	4	US-09-551-853D-2	Sequence 2, Appli	815	64.5	4.6	539	4	US-09-518-959-9	Sequence 9, Appli
743	65	4.7	518	4	US-09-215-450-19	Sequence 19, Appl	816	64.5	4.6	549	4	US-09-115-150-4	Sequence 4, Appli
744	65	4.7	518	4	US-09-416-901B-2	Sequence 2, Appli	817	64.5	4.6	549	4	US-09-489-039A-8237	Sequence 8237, Ap
745	65	4.7	518	4	US-09-548-376D-2	Sequence 2, Appli	818	64.5	4.6	550	4	US-09-721-870-18	Sequence 18, Appl
746	65	4.7	518	4	US-09-886-143-2	Sequence 2, Appli	819	64.5	4.6	555	4	US-09-543-681A-4582	Sequence 4582, Ap
747	65	4.7	518	4	US-09-794-927A-2	Sequence 2, Appli	820	64.5	4.6	561	4	US-09-134-000C-4759	Sequence 4759, Ap
748	65	4.7	518	4	US-09-548-373D-2	Sequence 2, Appli	821	64.5	4.6	604	4	US-09-820-809-13	Sequence 13, Appl
749	65	4.7	518	4	US-09-795-847B-2	Sequence 2, Appli	822	64.5	4.6	613	4	US-09-328-352-7962	Sequence 7962, Ap
750	65	4.7	518	4	US-09-869-414-2	Sequence 2, Appli	823	64.5	4.6	672	1	US-07-841-651-2	Sequence 2, Appli
751	65	4.7	518	4	US-09-548-366F-2	Sequence 2, Appli	824	64.5	4.6	672	1	US-07-841-651-3	Sequence 3, Appli
752	65	4.7	518	4	US-09-548-368D-2	Sequence 2, Appli	825	64.5	4.6	674	4	US-09-540-236-3546	Sequence 3546, Ap
753	65	4.7	518	4	US-09-794-925A-2	Sequence 2, Appli	826	64.5	4.6	677	4	US-09-543-681A-6388	Sequence 6388, Ap
754	65	4.7	518	4	US-09-806-194A-2	Sequence 2, Appli	827	64.5	4.6	723	4	US-09-248-796A-15245	Sequence 15245, A
755	65	4.7	535	4	US-09-489-039A-13906	Sequence 13906, A	828	64.5	4.6	742	4	US-09-902-540-11489	Sequence 11489, A
756	65	4.7	541	2	US-08-967-101-166	Sequence 166, App	829	64.5	4.6	870	4	US-09-949-016-11434	Sequence 11434, A
757	65	4.7	541	2	US-08-592-541-166	Sequence 166, App	830	64.5	4.6	878	4	US-09-949-016-11109	Sequence 11109, A

831	64.5	4.6	908	1	US-07-903-456-2	Sequence 2, Appli	904	64	4.6	846	4	US-09-949-016-10381	Sequence 10381, A
832	64.5	4.6	908	3	US-08-666-221B-6	Sequence 6, Appli	905	64	4.6	1042	4	US-09-512-250C-32	Sequence 32, Appl
833	64.5	4.6	908	3	US-08-249-241-2	Sequence 2, Appli	906	64	4.6	1063	4	US-09-248-796A-14361	Sequence 14361, A
834	64.5	4.6	908	4	US-09-949-016-7025	Sequence 7025, Ap	907	64	4.6	1278	4	US-09-462-136-2	Sequence 2, Appli
835	64.5	4.6	912	5	PCT-US91-09422-19	Sequence 19, Appl	908	64	4.6	1318	4	US-09-949-016-10152	Sequence 10152, A
836	64.5	4.6	1071	2	US-08-975-527-1	Sequence 1, Appli	909	64	4.6	1551	4	US-09-437-568A-46	Sequence 46, Appl
837	64.5	4.6	1122	4	US-09-489-039A-8554	Sequence 8554, Ap	910	63.5	4.6	175	3	US-08-858-207A-363	Sequence 363, App
838	64	4.6	125	4	US-09-270-767-36480	Sequence 36480, A	911	63.5	4.6	221	4	US-09-248-796A-16290	Sequence 16290, A
839	64	4.6	125	4	US-09-270-767-51697	Sequence 51697, A	912	63.5	4.6	232	4	US-09-902-540-12730	Sequence 12730, A
840	64	4.6	135	4	US-09-270-767-32080	Sequence 32080, A	913	63.5	4.6	237	3	US-08-768-859A-21	Sequence 21, Appl
841	64	4.6	171	4	US-09-902-540-10737	Sequence 10737, A	914	63.5	4.6	237	3	US-08-767-820A-21	Sequence 21, Appl
842	64	4.6	179	4	US-09-902-540-11797	Sequence 11797, A	915	63.5	4.6	237	3	US-08-622-046B-1	Sequence 1, Appli
843	64	4.6	205	4	US-09-540-236-2955	Sequence 2955, Ap	916	63.5	4.6	237	3	US-09-100-264-12	Sequence 12, Appli
844	64	4.6	238	3	US-09-247-155-89	Sequence 89, Appl	917	63.5	4.6	237	4	US-08-843-076D-8	Sequence 8, Appli
845	64	4.6	250	4	US-09-543-681A-4487	Sequence 4487, Ap	918	63.5	4.6	244	3	US-08-622-046B-5	Sequence 5, Appli
846	64	4.6	258	4	US-09-328-352-4425	Sequence 4425, Ap	919	63.5	4.6	247	4	US-09-489-039A-8478	Sequence 8478, Ap
847	64	4.6	264	4	US-09-107-532A-5290	Sequence 5290, Ap	920	63.5	4.6	250	3	US-09-134-001C-4399	Sequence 4399, Ap
848	64	4.6	296	4	US-09-724-623-103	Sequence 103, App	921	63.5	4.6	250	4	US-09-949-016-10962	Sequence 10962, A
849	64	4.6	315	3	US-09-134-001C-3561	Sequence 3561, Ap	922	63.5	4.6	261	3	US-08-768-859A-19	Sequence 19, Appl
850	64	4.6	332	2	US-08-671-978A-8	Sequence 8, Appli	923	63.5	4.6	261	3	US-08-767-820A-19	Sequence 19, Appl
851	64	4.6	344	3	US-09-110-116-4	Sequence 4, Appli	924	63.5	4.6	261	3	US-08-622-046B-3	Sequence 3, Appli
852	64	4.6	355	4	US-09-170-496D-164	Sequence 164, App	925	63.5	4.6	279	4	US-09-252-991A-24283	Sequence 24283, A
853	64	4.6	369	4	US-08-462-509B-4	Sequence 4, Appli	926	63.5	4.6	288	3	US-09-372-448A-2	Sequence 2, Appli
854	64	4.6	369	5	PCT-US95-05616-4	Sequence 4, Appli	927	63.5	4.6	289	3	US-09-372-422A-2	Sequence 2, Appli
855	64	4.6	371	4	US-09-328-352-7132	Sequence 7132, Ap	928	63.5	4.6	309	4	US-09-902-540-11246	Sequence 11246, A
856	64	4.6	372	4	US-08-462-509B-6	Sequence 6, Appli	929	63.5	4.6	311	4	US-09-489-039A-13013	Sequence 13013, A
857	64	4.6	374	3	US-09-045-583-48	Sequence 48, Appl	930	63.5	4.6	328	4	US-09-489-039A-10986	Sequence 10986, A
858	64	4.6	374	4	US-09-534-185-48	Sequence 48, Appl	931	63.5	4.6	332	4	US-09-252-991A-29029	Sequence 29029, A
859	64	4.6	377	5	PCT-US95-05616-6	Sequence 6, Appli	932	63.5	4.6	332	4	US-09-252-991A-31791	Sequence 31791, A
860	64	4.6	380	3	US-09-097-889-25	Sequence 25, Appl	933	63.5	4.6	345	4	US-09-248-796A-20780	Sequence 20780, A
861	64	4.6	380	4	US-09-098-079-25	Sequence 25, Appl	934	63.5	4.6	356	4	US-08-567-882-7	Sequence 7, Appli
862	64	4.6	386	4	US-09-813-133A-2	Sequence 2, Appli	935	63.5	4.6	359	4	US-09-248-796A-17633	Sequence 17633, A
863	64	4.6	386	4	US-09-248-796A-16627	Sequence 16627, A	936	63.5	4.6	378	4	US-09-540-236-3528	Sequence 3528, Ap
864	64	4.6	386	4	US-10-212-877-2	Sequence 2, Appli	937	63.5	4.6	379	1	US-08-227-108-18	Sequence 18, Appl
865	64	4.6	389	2	US-08-846-705-2	Sequence 2, Appli	938	63.5	4.6	379	2	US-09-073-674-18	Sequence 18, Appl
866	64	4.6	389	4	US-09-211-823C-23	Sequence 23, Appl	939	63.5	4.6	391	4	US-09-489-039A-9791	Sequence 9791, Ap
867	64	4.6	394	4	US-09-710-279-3292	Sequence 3292, Ap	940	63.5	4.6	404	2	US-08-428-243-7	Sequence 7, Appli
868	64	4.6	398	4	US-09-489-039A-13159	Sequence 13159, A	941	63.5	4.6	404	5	PCT-US93-10301-7	Sequence 7, Appli
869	64	4.6	402	3	US-08-846-704-4	Sequence 4, Appli	942	63.5	4.6	405	4	US-09-248-796A-17965	Sequence 17965, A
870	64	4.6	402	4	US-08-462-509B-2	Sequence 2, Appli	943	63.5	4.6	414	4	US-09-489-039A-10869	Sequence 10869, A
871	64	4.6	402	5	PCT-US95-05616-2	Sequence 2, Appli	944	63.5	4.6	430	4	US-09-583-110-4230	Sequence 4230, Ap
872	64	4.6	415	4	US-09-134-000C-4092	Sequence 4092, Ap	945	63.5	4.6	430	4	US-09-248-796A-14556	Sequence 14556, A
873	64	4.6	425	3	US-08-846-704-2	Sequence 2, Appli	946	63.5	4.6	437	4	US-09-107-433-3678	Sequence 3678, Ap
874	64	4.6	425	3	US-09-479-128-2	Sequence 2, Appli	947	63.5	4.6	449	4	US-09-949-016-8594	Sequence 8594, Ap
875	64	4.6	425	4	US-09-211-823C-22	Sequence 22, Appl	948	63.5	4.6	457	4	US-09-721-870-26	Sequence 26, Appl
876	64	4.6	425	4	US-09-826-509-549	Sequence 549, App	949	63.5	4.6	458	4	US-09-328-352-5083	Sequence 5083, Ap
877	64	4.6	428	4	US-09-345-236B-62	Sequence 62, Appl	950	63.5	4.6	470	4	US-09-543-681A-4625	Sequence 4625, Ap
878	64	4.6	430	1	US-08-601-435-2	Sequence 2, Appli	951	63.5	4.6	473	1	US-08-439-131A-4	Sequence 4, Appli
879	64	4.6	430	2	US-08-931-047-2	Sequence 2, Appli	952	63.5	4.6	473	1	US-08-440-674-3	Sequence 3, Appli
880	64	4.6	430	2	US-08-783-202-2	Sequence 2, Appli	953	63.5	4.6	473	4	US-08-879-337-7	Sequence 7, Appli
881	64	4.6	430	4	US-09-443-041A-31	Sequence 31, Appl	954	63.5	4.6	476	4	US-09-489-039A-10203	Sequence 10203, A
882	64	4.6	441	4	US-09-583-110-4400	Sequence 4400, Ap	955	63.5	4.6	482	4	US-09-328-352-7784	Sequence 7784, Ap
883	64	4.6	445	4	US-09-107-433-5039	Sequence 5039, Ap	956	63.5	4.6	488	1	US-08-115-365-2	Sequence 2, Appli
884	64	4.6	450	3	US-09-134-001C-4858	Sequence 4858, Ap	957	63.5	4.6	488	1	US-08-586-897-2	Sequence 2, Appli
885	64	4.6	450	4	US-09-252-991A-28134	Sequence 28134, A	958	63.5	4.6	488	4	US-09-826-509-561	Sequence 561, App
886	64	4.6	452	4	US-09-489-039A-12558	Sequence 12558, A	959	63.5	4.6	521	3	US-08-956-322-4	Sequence 4, Appli
887	64	4.6	458	1	US-09-041-075A-11	Sequence 11, Appl	960	63.5	4.6	531	4	US-08-956-322-4	Sequence 4, Appli
888	64	4.6	476	3	US-09-134-001C-3778	Sequence 3778, Ap	961	63.5	4.6	534	4	US-09-489-039A-9781	Sequence 9781, Ap
889	64	4.6	495	4	US-09-359-167-2	Sequence 2, Appli	962	63.5	4.6	542	4	US-09-710-279-920	Sequence 920, App
890	64	4.6	495	4	US-09-915-181A-7	Sequence 7, Appli	963	63.5	4.6	557	4	US-09-830-123-2	Sequence 2, Appli
891	64	4.6	501	4	US-09-328-352-6371	Sequence 6371, Ap	964	63.5	4.6	571	4	US-09-902-540-12884	Sequence 12884, A
892	64	4.6	522	4	US-09-902-540-12496	Sequence 12496, A	965	63.5	4.6	600	4	US-09-248-796A-20375	Sequence 20375, A
893	64	4.6	533	1	US-08-294-872-2	Sequence 2, Appli	966	63.5	4.6	650	3	US-09-902-540-14821	Sequence 14821, A
894	64	4.6	533	5	PCT-US95-09823-2	Sequence 2, Appli	967	63.5	4.6	652	3	US-08-800-291B-4	Sequence 4, Appli
895	64	4.6	536	4	US-09-359-167-8	Sequence 8, Appli	968	63.5	4.6	652	3	US-09-110-116-1	Sequence 1, Appli
896	64	4.6	585	4	US-09-949-016-7705	Sequence 7705, Ap	969	63.5	4.6	658	4	US-08-956-322-2	Sequence 2, Appli
897	64	4.6	613	4	US-09-107-532A-6935	Sequence 6935, Ap	970	63.5	4.6	658	4	US-09-492-709A-352	Sequence 352, App
898	64	4.6	615	4	US-09-107-532A-6507	Sequence 6507, Ap	971	63.5	4.6	685	4	US-09-538-092-1190	Sequence 1190, Ap
899	64	4.6	671	4	US-09-328-352-7868	Sequence 7868, Ap	972	63.5	4.6	689	4	US-09-720-317A-31	Sequence 31, Appl
900	64	4.6	696	4	US-09-107-532A-4163	Sequence 4163, Ap	973	63.5	4.6	790	4	US-09-248-796A-15264	Sequence 15264, A
901	64	4.6	771	4	US-09-252-991A-23521	Sequence 23521, A	974	63.5	4.6	803	4	US-09-543-681A-5459	Sequence 5459, Ap
902	64	4.6	816	4	US-09-248-796A-20939	Sequence 20939, A	975	63.5	4.6	850	4	US-09-543-681A-6767	Sequence 6767, Ap
903	64	4.6	823	4	US-09-949-016-6852	Sequence 6852, Ap	976	63.5	4.6	861	4	US-09-583-110-4394	Sequence 4394, Ap
												US-09-107-433-2860	Sequence 2860, Ap

977	63.5	4.6	923	3	US-09-397-885-1	Sequence 1, Appli	1050	63	4.5	683	4	US-08-979-847B-210	Sequence 210, App
978	63.5	4.6	923	4	US-09-969-362-1	Sequence 1, Appli	1051	63	4.5	849	3	US-08-804-439A-17	Sequence 17, Appl
979	63.5	4.6	1065	4	US-09-221-013A-10	Sequence 10, Appl	1052	63	4.5	849	3	US-08-720-229-17	Sequence 17, Appl
980	63.5	4.6	1098	3	US-08-726-214-10	Sequence 10, Appl	1053	63	4.5	852	4	US-09-319-588C-18	Sequence 18, Appl
981	63.5	4.6	1895	2	US-08-619-554-4	Sequence 4, Appli	1054	63	4.5	970	4	US-09-795-927-7	Sequence 7, Appli
982	63.5	4.6	2522	3	US-09-251-645-13	Sequence 13, Appl	1055	63	4.5	1076	4	US-10-160-719A-58	Sequence 58, Appl
983	63	4.5	138	4	US-09-583-110-4890	Sequence 4890, Ap	1056	63	4.5	1079	4	US-09-489-039A-7502	Sequence 7502, Ap
984	63	4.5	143	4	US-09-107-433-4477	Sequence 4477, Ap	1057	63	4.5	1168	4	US-09-313-942-24	Sequence 24, Appl
985	63	4.5	154	4	US-09-248-796A-20059	Sequence 20059, A	1058	63	4.5	2227	3	US-08-475-886-4	Sequence 4, Appli
986	63	4.5	175	4	US-09-543-681A-8328	Sequence 8328, Ap	1059	63	4.5	2227	3	US-08-475-886-6	Sequence 6, Appli
987	63	4.5	214	4	US-09-107-532A-5408	Sequence 5408, Ap	1060	63	4.5	2227	3	US-08-397-232-4	Sequence 4, Appli
988	63	4.5	219	1	US-08-186-529-4	Sequence 4, Appli	1061	63	4.5	2227	4	US-09-653-499-4	Sequence 4, Appli
989	63	4.5	219	1	US-08-640-386A-4	Sequence 4, Appli	1062	63	4.5	2227	4	US-09-653-499-6	Sequence 6, Appli
990	63	4.5	249	4	US-09-902-540-13089	Sequence 13089, A	1063	63	4.5	2227	4	US-10-135-988-6	Sequence 4, Appli
991	63	4.5	250	4	US-09-107-532A-6270	Sequence 6270, Ap	1064	63	4.5	2227	4	US-10-135-988-6	Sequence 6, Appli
992	63	4.5	253	1	US-08-265-087-4	Sequence 4, Appli	1065	63	4.5	2368	1	US-08-198-446B-15	Sequence 15, Appl
993	63	4.5	253	1	US-08-621-493-4	Sequence 4, Appli	1066	63	4.5	2368	2	US-08-870-693-15	Sequence 15, Appl
994	63	4.5	253	2	US-08-684-687-4	Sequence 4, Appli	1067	63	4.5	2910	1	US-08-466-033-183	Sequence 183, App
995	63	4.5	253	2	US-08-965-688-4	Sequence 4, Appli	1068	63	4.5	2910	2	US-08-444-733-183	Sequence 183, App
996	63	4.5	253	3	US-09-260-173-4	Sequence 4, Appli	1069	63	4.5	2910	2	US-08-464-134-183	Sequence 183, App
997	63	4.5	253	4	US-09-924-703-6	Sequence 6, Appli	1070	63	4.5	2910	2	US-08-461-361-183	Sequence 183, App
998	63	4.5	259	4	US-09-328-352-6237	Sequence 6237, Ap	1071	63	4.5	2910	2	US-08-485-910-183	Sequence 183, App
999	63	4.5	259	4	US-09-602-777A-292	Sequence 292, App	1072	63	4.5	2910	5	PCT-US95-06266-157	Sequence 157, App
1000	63	4.5	273	4	US-09-949-016-8333	Sequence 8333, Ap	1073	62.5	4.5	117	4	US-09-422-569-10	Sequence 10, Appl
1001	63	4.5	279	4	US-09-489-039A-13210	Sequence 13210, A	1074	62.5	4.5	117	4	US-09-823-153-2	Sequence 2, Appli
1002	63	4.5	284	4	US-09-270-767-33635	Sequence 33635, A	1075	62.5	4.5	131	4	US-09-902-540-12460	Sequence 12460, A
1003	63	4.5	284	4	US-09-270-767-48852	Sequence 48852, A	1076	62.5	4.5	164	4	US-09-902-540-10754	Sequence 10754, A
1004	63	4.5	287	4	US-09-134-000C-5944	Sequence 5944, Ap	1077	62.5	4.5	176	4	US-09-248-796A-15652	Sequence 15652, A
1005	63	4.5	289	4	US-09-540-236-2019	Sequence 2019, Ap	1078	62.5	4.5	202	3	US-09-134-001C-5617	Sequence 5617, Ap
1006	63	4.5	290	4	US-09-910-174B-8	Sequence 8, Appli	1079	62.5	4.5	207	4	US-09-543-681A-7271	Sequence 7271, Ap
1007	63	4.5	290	4	US-09-620-461-8	Sequence 8, Appli	1080	62.5	4.5	232	4	US-09-107-532A-3905	Sequence 3905, Ap
1008	63	4.5	290	4	US-09-451-291-1	Sequence 1, Appli	1081	62.5	4.5	234	4	US-09-710-279-2580	Sequence 2580, Ap
1009	63	4.5	290	4	US-09-645-069-4	Sequence 4, Appli	1082	62.5	4.5	237	1	US-08-096-946-10	Sequence 10, Appl
1010	63	4.5	299	4	US-09-583-110-2991	Sequence 2991, Ap	1083	62.5	4.5	237	3	US-08-768-859A-16	Sequence 16, Appl
1011	63	4.5	345	4	US-09-362-123A-2	Sequence 2, Appli	1084	62.5	4.5	237	3	US-08-767-820A-16	Sequence 16, Appl
1012	63	4.5	345	4	US-09-107-532A-4426	Sequence 4426, Ap	1085	62.5	4.5	237	3	US-08-622-046B-12	Sequence 12, Appl
1013	63	4.5	346	4	US-09-149-476-493	Sequence 493, App	1086	62.5	4.5	237	3	US-08-944-483-37	Sequence 37, Appl
1014	63	4.5	350	4	US-09-902-540-14418	Sequence 14418, A	1087	62.5	4.5	237	3	US-09-100-264-1	Sequence 1, Appli
1015	63	4.5	354	4	US-09-270-767-45287	Sequence 45287, A	1088	62.5	4.5	237	4	US-08-843-076D-1	Sequence 1, Appli
1016	63	4.5	361	4	US-09-543-681A-5180	Sequence 5180, Ap	1089	62.5	4.5	237	5	PCT-US94-07329-10	Sequence 10, Appl
1017	63	4.5	365	2	US-08-833-610-7	Sequence 7, Appli	1090	62.5	4.5	237	5	PCT-US95-06157-16	Sequence 16, Appl
1018	63	4.5	365	3	US-08-834-033A-17	Sequence 17, Appl	1091	62.5	4.5	238	3	US-08-768-859A-8	Sequence 8, Appli
1019	63	4.5	365	4	US-09-377-452-7	Sequence 17, Appl	1092	62.5	4.5	238	3	US-08-767-820A-8	Sequence 8, Appli
1020	63	4.5	374	4	US-09-721-341-8	Sequence 7, Appli	1093	62.5	4.5	238	5	PCT-US95-06157-8	Sequence 8, Appli
1021	63	4.5	374	4	US-09-721-495B-8	Sequence 8, Appli	1094	62.5	4.5	244	3	US-08-768-859A-10	Sequence 10, Appl
1022	63	4.5	387	4	US-09-549-848B-17	Sequence 8, Appli	1095	62.5	4.5	244	3	US-08-767-820A-10	Sequence 10, Appl
1023	63	4.5	391	4	US-09-710-279-1236	Sequence 17, Appl	1096	62.5	4.5	244	3	US-08-622-046B-16	Sequence 16, Appl
1024	63	4.5	398	4	US-09-328-352-6411	Sequence 1236, Ap	1097	62.5	4.5	244	3	US-08-622-046B-16	Sequence 16, Appl
1025	63	4.5	401	4	US-09-489-039A-9416	Sequence 9416, Ap	1098	62.5	4.5	244	4	US-09-100-264-5	Sequence 5, Appli
1026	63	4.5	422	3	US-09-134-001C-4048	Sequence 4048, Ap	1099	62.5	4.5	244	5	PCT-US95-06157-10	Sequence 10, Appl
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1028	63	4.5	425	4	US-09-543-681A-6042	Sequence 6042, Ap	1101	62.5	4.5	261	3	US-08-767-820A-6	Sequence 6, Appli
1029	63	4.5	430	4	US-09-443-041A-18	Sequence 18, Appl	1102	62.5	4.5	261	3	US-08-622-046B-14	Sequence 14, Appl
1030	63	4.5	430	4	US-09-134-000C-4627	Sequence 4627, Ap	1103	62.5	4.5	261	3	US-09-100-264-7	Sequence 7, Appli
1031	63	4.5	438	2	US-08-677-049-9	Sequence 9, Appli	1104	62.5	4.5	261	3	US-08-983-075D-7	Sequence 7, Appli
1032	63	4.5	443	1	US-08-570-157-6	Sequence 6, Appli	1105	62.5	4.5	261	4	US-08-843-076D-3	Sequence 3, Appli
1033	63	4.5	443	3	US-09-076-510-6	Sequence 6, Appli	1106	62.5	4.5	261	5	PCT-US95-06157-6	Sequence 6, Appli
1034	63	4.5	443	4	US-09-004-349-6	Sequence 4, Appli	1107	62.5	4.5	276	3	US-09-134-001C-3456	Sequence 3456, Ap
1035	63	4.5	461	1	US-08-194-338-4	Sequence 4, Appli	1108	62.5	4.5	277	1	US-08-118-270-68	Sequence 68, Appl
1036	63	4.5	468	2	US-08-959-011-3	Sequence 3, Appli	1109	62.5	4.5	277	5	PCT-US93-08528-68	Sequence 68, Appl
1037	63	4.5	478	4	US-09-107-532A-6105	Sequence 6105, Ap	1110	62.5	4.5	278	4	US-09-949-016-7711	Sequence 7711, Ap
1038	63	4.5	478	4	US-09-949-016-6543	Sequence 6543, Ap	1111	62.5	4.5	283	4	US-09-134-000C-4870	Sequence 4870, Ap
1039	63	4.5	485	4	US-09-949-016-10465	Sequence 10465, A	1112	62.5	4.5	291	4	US-09-393-634-64	Sequence 64, Appl
1040	63	4.5	497	4	US-09-248-796A-20395	Sequence 20395, A	1113	62.5	4.5	291	4	US-09-949-016-6919	Sequence 6919, Ap
1041	63	4.5	506	4	US-09-543-681A-8246	Sequence 8246, Ap	1114	62.5	4.5	291	4	US-09-949-016-8213	Sequence 8213, Ap
1042	63	4.5	521	3	US-09-134-001C-4290	Sequence 4290, Ap	1115	62.5	4.5	292	4	US-09-543-681A-7918	Sequence 7918, Ap
1043	63	4.5	554	4	US-09-540-236-2634	Sequence 2634, Ap	1116	62.5	4.5	304	4	US-09-328-352-7098	Sequence 7098, Ap
1044	63	4.5	580	4	US-09-657-252-2	Sequence 2, Appli	1117	62.5	4.5	323	4	US-09-540-236-2883	Sequence 2883, Ap
1045	63	4.5	597	4	US-09-328-352-4703	Sequence 4703, Ap	1118	62.5	4.5	324	4	US-09-543-681A-5947	Sequence 5947, Ap
1046	63	4.5	611	2	US-08-677-049-2	Sequence 2, Appli	1119	62.5	4.5	325	4	US-09-107-532A-6542	Sequence 6542, Ap
1047	63	4.5	629	4	US-09-252-991A-17988	Sequence 17988, A	1120	62.5	4.5	332	4	US-09-252-991A-18980	Sequence 18980, A
1048	63	4.5	659	4	US-09-252-991A-30353	Sequence 30353, A	1121	62.5	4.5	332	4	US-09-252-991A-31150	Sequence 31150, A
1049	63	4.5	683	4	US-08-979-847B-208	Sequence 208, App	1122	62.5	4.5	332	4	US-09-949-016-6161	Sequence 6161, Ap

1123	62.5	4.5	351	4	US-09-949-016-11252	Sequence 11252, A	1196	62.5	4.5	687	4	US-09-543-681A-5839	Sequence 5839, Ap
1124	62.5	4.5	351	4	US-09-949-016-11253	Sequence 11253, A	1197	62.5	4.5	702	4	US-09-328-352-4189	Sequence 4189, Ap
1125	62.5	4.5	355	4	US-09-328-352-4374	Sequence 4374, Ap	1198	62.5	4.5	734	4	US-09-252-991A-33036	Sequence 33036, A
1126	62.5	4.5	361	3	US-09-248-568-2	Sequence 2, Appli	1199	62.5	4.5	784	4	US-09-489-039A-14075	Sequence 14075, A
1127	62.5	4.5	361	4	US-09-364-425B-19	Sequence 19, Appl	1200	62.5	4.5	822	4	US-09-248-796A-20139	Sequence 20139, A
1128	62.5	4.5	361	4	US-09-364-425B-50	Sequence 50, Appl	1201	62.5	4.5	877	1	US-08-486-270-12	Sequence 12, Appl
1129	62.5	4.5	371	4	US-09-636-215-708	Sequence 708, App	1202	62.5	4.5	877	3	US-08-367-264-12	Sequence 12, Appl
1130	62.5	4.5	371	4	US-09-685-166A-708	Sequence 708, App	1203	62.5	4.5	877	4	US-09-153-757-12	Sequence 12, Appl
1131	62.5	4.5	371	4	US-09-679-426-708	Sequence 708, App	1204	62.5	4.5	877	4	US-09-459-715-12	Sequence 12, Appl
1132	62.5	4.5	371	4	US-09-759-143-708	Sequence 708, App	1205	62.5	4.5	883	1	US-08-106-433A-2	Sequence 2, Appli
1133	62.5	4.5	371	4	US-09-651-236-708	Sequence 708, App	1206	62.5	4.5	883	3	US-09-254-352B-16	Sequence 16, Appl
1134	62.5	4.5	373	4	US-09-107-532A-7048	Sequence 7048, Ap	1207	62.5	4.5	889	1	US-08-118-101A-4	Sequence 4, Appli
1135	62.5	4.5	376	4	US-09-949-016-7545	Sequence 7545, Ap	1208	62.5	4.5	908	3	US-08-823-110-1	Sequence 1, Appli
1136	62.5	4.5	380	4	US-09-149-045-2	Sequence 2, Appli	1209	62.5	4.5	908	3	US-08-604-298-1	Sequence 1, Appli
1137	62.5	4.5	382	4	US-09-252-991A-32165	Sequence 32165, A	1210	62.5	4.5	919	3	US-08-377-503-2	Sequence 2, Appli
1138	62.5	4.5	392	4	US-09-489-039A-12520	Sequence 12520, A	1211	62.5	4.5	919	3	US-08-178-019-2	Sequence 2, Appli
1139	62.5	4.5	398	4	US-09-328-352-6136	Sequence 6136, Ap	1212	62.5	4.5	987	4	US-09-949-016-10265	Sequence 10265, A
1140	62.5	4.5	400	4	US-09-636-215-852	Sequence 852, App	1213	62.5	4.5	1032	4	US-09-332-522E-94	Sequence 94, Appl
1141	62.5	4.5	400	4	US-09-685-166A-852	Sequence 852, App	1214	62.5	4.5	1094	4	US-10-160-719A-26	Sequence 26, Appl
1142	62.5	4.5	400	4	US-09-679-426-852	Sequence 852, App	1215	62.5	4.5	1094	4	US-10-160-719A-46	Sequence 46, Appl
1143	62.5	4.5	400	4	US-09-759-143-852	Sequence 852, App	1216	62.5	4.5	1158	4	US-09-313-942-26	Sequence 26, Appl
1144	62.5	4.5	400	4	US-09-651-236-852	Sequence 852, App	1217	62.5	4.5	1248	4	US-10-042-810-2	Sequence 2, Appli
1145	62.5	4.5	405	4	US-09-489-039A-9411	Sequence 9411, Ap	1218	62.5	4.5	1278	4	US-10-042-810-4	Sequence 4, Appli
1146	62.5	4.5	409	4	US-09-328-352-5147	Sequence 5147, Ap	1219	62.5	4.5	1338	4	US-09-631-603-2	Sequence 2, Appli
1147	62.5	4.5	415	4	US-09-603-208A-286	Sequence 286, App	1220	62.5	4.5	1765	4	US-09-270-767-45587	Sequence 45587, A
1148	62.5	4.5	424	4	US-09-489-039A-9628	Sequence 9628, Ap	1221	62.5	4.5	1849	4	US-08-851-567B-49	Sequence 49, Appl
1149	62.5	4.5	437	4	US-09-248-796A-16548	Sequence 16548, A	1222	62.5	4.5	2516	4	US-08-851-567B-47	Sequence 47, Appl
1150	62.5	4.5	437	4	US-09-830-433A-59	Sequence 59, Appl	1223	62.5	4.5	2516	4	US-09-817-514A-2	Sequence 2, Appli
1151	62.5	4.5	451	4	US-09-446-861-127	Sequence 127, App	1224	62	4.5	103	4	US-09-543-681A-7951	Sequence 7951, Ap
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1153	62.5	4.5	455	4	US-09-543-681A-5989	Sequence 5989, Ap	1226	62	4.5	152	4	US-09-710-279-2224	Sequence 2224, Ap
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1169	62.5	4.5	553	3	US-09-020-956-113	Sequence 113, App	1242	62	4.5	242	6	5455030-15	Patent No. 5455030
1170	62.5	4.5	553	3	US-09-030-607-113	Sequence 113, App	1243	62	4.5	242	6	5455030-15	Patent No. 5455030
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1446 61.5 4.4 420 4 US-09-107-532A-4006 Sequence 4006, Ap
1447 61.5 4.4 421 4 US-09-489-039A-7699 Sequence 7699, Ap
1448 61.5 4.4 422 1 US-07-996-772A-12 Sequence 12, Appl
1449 61.5 4.4 425 4 US-09-134-000C-3951 Sequence 3951, Ap
1450 61.5 4.4 427 4 US-09-543-681A-6225 Sequence 6225, Ap
1451 61.5 4.4 435 2 US-08-031-538-11 Sequence 11, Appl
1452 61.5 4.4 435 4 US-09-489-039A-13740 Sequence 13740, A
1453 61.5 4.4 437 4 US-09-830-433A-12 Sequence 12, Appl
1454 61.5 4.4 440 4 US-09-071-035-370 Sequence 370, App
1455 61.5 4.4 441 4 US-09-540-236-2016 Sequence 2016, Ap
1456 61.5 4.4 444 4 US-09-540-236-1993 Sequence 1993, Ap
1457 61.5 4.4 445 2 US-08-157-185-2 Sequence 2, Appli
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1459 61.5 4.4 445 3 US-09-450-797-2 Sequence 2, Appli
1460 61.5 4.4 445 3 US-09-328-314-16 Sequence 16, Appl
1461 61.5 4.4 445 3 US-09-450-790A-2 Sequence 2, Appli
1462 61.5 4.4 445 4 US-09-332-837-2 Sequence 2, Appli
1463 61.5 4.4 445 4 US-09-826-509-451 Sequence 451, App
1464 61.5 4.4 445 5 PCT-US93-10553-2 Sequence 2, Appli
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1466 61.5 4.4 473 4 US-09-252-991A-19484 Sequence 19484, A
1467 61.5 4.4 490 4 US-09-489-039A-9610 Sequence 9610, Ap
1468 61.5 4.4 493 4 US-09-540-236-2120 Sequence 2120, Ap
1469 61.5 4.4 509 4 US-09-902-540-9976 Sequence 9976, Ap
1470 61.5 4.4 513 3 US-09-097-889-15 Sequence 15, Appl
1471 61.5 4.4 513 4 US-09-098-079-15 Sequence 15, Appl
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1474 61.5 4.4 540 2 US-08-751-767A-10 Sequence 10, Appl
1475 61.5 4.4 552 4 US-09-489-039A-7419 Sequence 7419, Ap
1476 61.5 4.4 553 3 US-08-630-172-13 Sequence 13, Appl
1477 61.5 4.4 553 3 US-09-375-419-13 Sequence 13, Appl
1478 61.5 4.4 575 4 US-09-949-016-8640 Sequence 8640, Ap
1479 61.5 4.4 590 4 US-09-489-039A-7412 Sequence 7412, Ap
1480 61.5 4.4 596 4 US-09-252-991A-26031 Sequence 26031, A
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1483 61.5 4.4 686 4 US-09-134-000C-5166 Sequence 5166, Ap
1484 61.5 4.4 701 4 US-09-328-352-5717 Sequence 5717, Ap
1485 61.5 4.4 790 4 US-09-543-681A-5847 Sequence 5847, Ap
1486 61.5 4.4 877 3 US-09-126-280-2 Sequence 2, Appli
1487 61.5 4.4 968 3 US-09-180-439-3 Sequence 3, Appli

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1489 61.5 4.4 1000 3 US-09-193-562D-30 Sequence 30, Appl
1490 61.5 4.4 1000 4 US-10-055-412B-30 Sequence 30, Appl
1491 61.5 4.4 1043 4 US-10-160-719A-50 Sequence 50, Appl
1492 61.5 4.4 1077 4 US-10-160-719A-6 Sequence 6, Appli
1493 61.5 4.4 1077 4 US-10-160-719A-30 Sequence 30, Appl
1494 61.5 4.4 1086 4 US-10-160-719A-18 Sequence 18, Appl
1495 61.5 4.4 1086 4 US-10-160-719A-38 Sequence 38, Appl
1496 61.5 4.4 1261 3 US-09-208-742-4 Sequence 4, Appli
1497 61.5 4.4 1261 3 US-09-332-295-2 Sequence 2, Appli
1498 61.5 4.4 1261 4 US-09-709-979-2 Sequence 2, Appli
1499 61.5 4.4 1261 4 US-10-147-268-2 Sequence 2, Appli
1500 61.5 4.4 1364 4 US-09-252-991A-26880 Sequence 26880, A

ALIGNMENTS

RESULT 1
US-09-663-600A-190
; Sequence 190, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 190
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
US-09-663-600A-190

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Best Local Similarity 99.6%; Pred. No. 1.le-146;
Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MWFFQGLSFLPSALVIWTSAAIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML 60

QY 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLISIVANFQKTLFAA 120
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Db 61 NIAAVLCIATIIYRYKQVHALSPEENVIIKLNKAGLVGLISIVANFQKTLFAA 120

QY 121 HVSGAVLTFGMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSVL 180
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Db 121 HVSGAVLTFGMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLLVICGVSALSMLTCSVL 180

QY 181 HSGNFGTDLQKLNHNPNEDKGYVLHMITTAAEWSMSFSFFGFFLTYYIRDFOKISLRVEAN 240
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; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTSA/AF
US-09-247-155-20

Query Match      8.5%; Score 118; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWWFQQGLSFLPSALVIWTSA 21
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Db 1 MWWFQQGLSFLPSALVIWTSA 21

RESULT 8
US-09-663-600A-20
; Sequence 20, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTSA/AF
US-09-663-600A-20

Query Match      8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWWFQQGLSFLPSALVIWTSA 21
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Db 1 MWWFQQGLSFLPSALVIWTSA 21

RESULT 9
US-09-621-976-2
; Sequence 2, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
```

```
;
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21..-1
US-09-621-976-2

Query Match      8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWWFQQGLSFLPSALVIWTSA 21
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Db 1 MWWFQQGLSFLPSALVIWTSA 21

RESULT 10
US-09-513-999C-2
; Sequence 2, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTSA/AF
US-09-513-999C-2

Query Match      8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWWFQQGLSFLPSALVIWTSA 21
  |||||
Db 1 MWWFQQGLSFLPSALVIWTSA 21

RESULT 11
US-09-471-276-2
; Sequence 2, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
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FILE REFERENCE: GENSET.025CP1
CURRENT APPLICATION NUMBER: US/09/471,276
CURRENT FILING DATE: 1999-12-21
EARLIER APPLICATION NUMBER: 09/057,719
EARLIER FILING DATE: 1998-04-09
EARLIER APPLICATION NUMBER: 09/069,047
EARLIER FILING DATE: 1998-04-28
EARLIER APPLICATION NUMBER: PCT/IB99/00712
EARLIER FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1622
SOFTWARE: Patent.pm
SEQ ID NO 2
LENGTH: 21
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: 1..21
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 5.5
OTHER INFORMATION: seq SFLPSALVIWTS/AF

US-09-471-276-2

Query Match 8.5%; Score 118; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MWWFQQLSFLPSALVIWTS 21

RESULT 12

US-09-107-532A-4147
Sequence 4147, Application US/09107532A
Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 4147:

SEQUENCE CHARACTERISTICS:

LENGTH: 291 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...291
SEQUENCE DESCRIPTION: SEQ ID NO: 4147:
US-09-107-532A-4147

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Best Local Similarity 22.9%; Pred. No. 0.088;
Matches 58; Conservative 26; Mismatches 88; Indels 81; Gaps 9;

QY 6 QGLSFLPSALV-----IWTSAAFIFSITAVTLHHIDPALPYISDTGTVAPEKCLFGAM 59
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QY 60 LNTAAVLCIATYVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTT--- 116
Db 89 --TAAVIGFVQRSRLKNDTAI-----GIVSSFFALGIILISYAQSATDLY 133

QY 117 -----LFAAHVSGAVLTFGMGSLYMFVQITLSYQMP---KIHGKQVFWI 158
Db 134 HILFGNVLAVRESDLLLTALVSGIVLIF---VFFPYKELKITSPDTMAKAYGLNTSLI 189

QY 159 RLLLVICGVSALSMLTSCSVLHSGNFGTDLEQKLHWNPEDKGY-----VLHMITTAAEW 213
Db 190 HYLMEF-----LTLVAVVSLQTVGTILVIAMLITPAATAYLLTNHLLKMIITAAGI 241

QY 214 SMSFSFFGFFLTY 226
Db 242 GMLSAVVGVFFSY 254

RESULT 13

US-09-721-870-14

Sequence 14, Application US/09721870
Patent No. 6632621

GENERAL INFORMATION:

APPLICANT: Lowery, David E.

APPLICANT: Geary, Timothy G.

APPLICANT: Kubiak, Teresa M.

APPLICANT: Larsen, Martha J.

TITLE OF INVENTION: MODULATORS OF G PROTEIN-COUPLED RECEPTORS

FILE REFERENCE: 28341/6223

CURRENT APPLICATION NUMBER: US/09/721,870

CURRENT FILING DATE: 2000-11-24

NUMBER OF SEQ ID NOS: 180

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14

LENGTH: 387

TYPE: PRT

ORGANISM: Homo sapiens

US-09-721-870-14

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Best Local Similarity 23.0%; Pred. No. 0.13;
Matches 50; Conservative 34; Mismatches 82; Indels 51; Gaps 11;

QY 69 ATIVRYKQVHALSPEENVIIKLNKAGLVGLSCLGLSIVANFQKTTLFAAH----- 121
Db 46 AVLYTMKH-RQLQTVQNIFILNCASNVLMCLTSLPITFITNVYKQWFFSPVCKLIPL 104

QY 122 VSGA---VLTFGMGSLYMFVQITLSYQMPKIHGKQVFWIRLLLVICGVSALSMLTCS 178
Db 105 VQGASIFVSTFSLSAIALDRYLVVRPHKQKLSRSAMMIAL--IW----VISVVVCM 158

QY 179 VLHSGNFGTDLE-QKL-----HWNPED--KGYVLHMITTAAEWSMSFSFFGFFLT 225
Db 159 -----YGWYMDVEKLNGLCCEYCSHWPPLAEVRKGYTFLVLIT----QFLFPFATMAFC 208

QY 226 YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLL 262

Db 65 LWWPWIFWLLSIGCWLTIIISMI--YIPPI THHKLSEYSEFFEKRIDPLGLTGTIGLIL 122

Qy 40 LPYISDTGTVAPEKCLFGAMLNIAAVLCIATIV--RYKQVHALSPEE----- 85

Db 123 FNFVWTQGPVVGWNTAYIIALLIIIAVLLIIVAFFIIELIYIAKYPLVPKSVFNLKIGMVLAC 182

Qy 86 -----NVIKLNK---AG-----LVLGILSCLGLSIVANFOKTTLF 118

Db 183 ISCGWGSFGIWQYYWNIIILNRKYTPIAGSLTYVPFLVMGIAAIASSIIISHTKPSYI 242

Qy 119 AAHVSGAVLTFMGSLYMFVQTIILSYQMOPKIHGKQVFWIRLLL---VIWCGVSALSMT 175

Db 243 ---ISFSTICFMVGCLMLSVTPI-----QQSYFRLTGQMFILCWAMDMSFPA 287

Qy 176 CSSVL-----HSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFG 221

Db 288 ASIILSDYLPNHHQGMAGS-----LVSTVINYSVSL-FLG 321

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GenCore version 5.1.6
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Post-processing: Minimum Match 0%
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Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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627	1392	100.0	266 14 US-10-063-742-2 Sequence 2, Appli
733	1392	100.0	266 15 US-10-264-237-2714 Sequence 2714, Ap
737	1392	100.0	266 15 US-10-621-401-147 Sequence 147, App
744	1392	100.0	266 17 US-10-972-317-2 Sequence 2, Appli
746	1392	100.0	267 10 US-09-305-736-147 Sequence 147, App
747	1392	100.0	267 10 US-09-818-683-147 Sequence 147, App
748	1392	100.0	267 11 US-09-818-683-147 Sequence 147, App
749	1392	100.0	275 15 US-10-276-774-2411 Sequence 2411, Ap
750	1388	99.7	267 11 US-09-978-360A-702 Sequence 702, App

751	1388	99.7	267	14	US-10-319-763-190	Sequence 190, App
752	595.5	42.8	172	14	US-10-319-763-96	Sequence 96, Appl
753	486.5	34.9	238	15	US-10-108-260A-2867	Sequence 2867, Ap
754	480.5	34.5	231	15	US-10-415-188-11	Sequence 11, Appl
755	461.5	33.2	246	15	US-10-243-552-975	Sequence 975, App
756	358	25.7	69	11	US-09-978-360A-736	Sequence 736, App
757	358	25.7	69	14	US-10-319-763-130	Sequence 130, App
758	358	25.7	69	14	US-10-319-763-224	Sequence 224, App
759	317.5	22.8	180	15	US-10-264-237-2144	Sequence 2144, Ap
760	251	18.0	132	16	US-10-755-889-453	Sequence 453, App
761	251	18.0	132	16	US-10-643-795A-100	Sequence 100, App
762	251	18.0	132	17	US-10-948-518-100	Sequence 100, App
763	214.5	15.4	283	15	US-10-243-552-521	Sequence 521, App
764	212	15.2	249	18	US-10-712-892A-37	Sequence 37, Appl
765	152	10.9	304	15	US-10-131-487A-83	Sequence 83, Appl
766	151.5	10.9	437	10	US-09-374-046A-66	Sequence 66, Appl
767	151.5	10.9	437	15	US-10-616-263-66	Sequence 66, Appl
768	126	9.1	63	15	US-10-243-552-618	Sequence 618, App
769	118	8.5	21	10	US-09-903-190-20	Sequence 20, Appl
770	118	8.5	21	14	US-10-319-763-20	Sequence 20, Appl
771	118	8.5	21	17	US-10-926-683-2	Sequence 2, Appli
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